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Post-processing: Minimum Match 0%
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Listing first 45
                                                                                                                                   Pred. No. is the number of results predicted by chance to have score greater than or equal to the score of the result being puand is derived by analysis of the total score distribution.
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                                                                                                                                                                                                            Nucleotide sequence of the ODD4b5.3 enzyme.
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  Hart DNJ
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Scoring table: Sequence: Perfect score: Run on: OM nucleic -

Database :

WPI; 1998-240074/21. P-PSDB; AAW56097.

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Query Match
Best Local Similarity
Matches 2563; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New isolated S-adenosyl-L-homocysteine hydrolase enzyme - is develop products which can be used in the treatment of e.g. auto-immune disease, transplantations or cancers
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        20-FEB-2001;
                                                                     Human; prostate pharmacogenomic
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                                                                                                                                              ABV23195 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               TCATTATCCAAGTTCTGCAGACCACACAGGAACTTGCTTCATGGCTCTTTAGATGAAATA
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                                                      sapiens.
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marker;
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13-DEC-2000;
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                                         AGGCGCCCAAGAAGCAAATCCAGTTTGCTGATGACATGCAGGAGTTCACCAAATTCCCCA
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
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The invention relates to an isolated nucleic acid molecule (I) come a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer (b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
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                                                                             also useful as a pharmacodyanamic or pharmacogenomic marker
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C. TARLARMAGE TARTAMATITEMACTACTACHAMATICACHACTITETTATA	GTCC 1	ATATGGGCCACTCCAACACAGAAATCGATGTGACCAGCCTCCGGACTCCGGAGCTGACGT 1500 	ATAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCA 1440 	GGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAA 1380 	TIGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGGATGG	TGTGTGGCTAIGGTGAGGTAGGCAAGGGCTGCTGTGCTCCTCAAAGCTCTTGGAGCAA 1260 	CCATTTIGGAIGGCCIGAAGAGGACCACAGAIGIGAIGITIGGIGGGAAACAAGIGGIGG 1200 	TGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCCGGCGAGAAT 1140 	TGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCA 1080 	GGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGAAGAGAGGGG 1020 	TGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACT 960 	CAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTG 900	CTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGGTTG 840 	CCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTG 780	GTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACACACATCACAG 720 	GACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAAC 660 	0 0	GTTCAGCTGCATCCTACACAGATAGCTCTGATGATGATGTTCTCCCCGAGAGAAGCAGC 610
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ABV29032;	, ω	2521 TCTAGGATTATTTCTGTTCTCCAAAAAAAAAAAAAAAAA	2461 GACTTGCTCATTTTTCGACTTTTAACTAGACTACACTCTATT 	2401 CTTG	2341 AGCC 2410 AGCC	2281 ACCT 2350 ACCT	2221 GCCC 1111 2290 GCCC	2230 (2101 GGTG	2041 0	2051 1	1921 TTTC 1991 TTTC	1861 CAAG	1801	1811 ATCT	1751 GAT	1621	1631

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                                                                                                                                                                                                                                                      patient;
(I) is ai
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 6147-6148; 11750pp; English.
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                            AGCCCTGTTTCCTGCGTAAAGGTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGG
                                                                  ACCTACCCGGCAGGTAGGTTAGATGTGGGTGGTGCATGTTAATTTCCCTTAGAAGTTCCA
                                                                                                    GCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAGAAGCAGGGATGGT
                                                                                                                   GCCCATTTCTTAGCTGCAAATCAGTGCTCTTTCACTTCTTCAGAGAAGCAGGGATGGT
                                                                                                                                             TCATTATCCAAGTTCTGCAGACCACACAGGAACTTGCTTCATGGCTCTTTAGATGAAATA
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                         CC This sequence encodes a human S-adenosyl-5-homocysteine hydrolase (SAHH).

CC The SAHH protein can be used to generate specific antibodies and in drug screening to identify specific binding agents. Antagonists of the comprohening to identify specific binding agents. Antagonists of the protein are used to treat or prevent a wide range of viral, bacterial, compared to treat or prevent a wide range of viral, bacterial, compared to treat or prevent a wide range of viral, bacterial, compared to treat or prevent a wide range of viral, bacterial, compared to the sequence of the sequences, and many autoimmune diseases (e.g. acquired immune deficiency syndrome, allergy, asthma, diabetes compilities, multiple sclerosis etc.). All these conditions may be treated by expressing antisense sequences, triplex-forming agents or ribozymes can be used against the nucleic acid. The nucleic acid and its fragments can be used as probes or primers for detecting and quantifying gene expression, for diagnosis or monitoring of disease, to identify genetic variations, mutations or polymorphisms, in gene mapping and as antisense therapeutics. Antibodies are used directly as antagonists, indirectly to disease in standard immunoassays, in competitive drug screens and to constant the protein from natural sources.
                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                         Nucleic acid encoding human S-adenosyl-5-homocysteine hydrolase for production of recombinant enzyme, useful for diagnosis, treatment and prevention of cancers, infections and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-094906/08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Corley: NC; ... Hillman JE;
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2073		Q B		QY 1250 TCTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATCTGTGCTGCTGCAGGCCTGCAT 1309	D •
2013		Ov D		QY 1190 ACAAGTGGTGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTGCTGCTCCTAAAGC 1249	n u
1953		o p cy	•	Qy 1130 CTGCCAGAATCCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAA 1189	U D
1893	150 CCTTATTAACAGGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTCAAATGCTAAAATGCTAAGACCATCTCAACAATCTCAAAAATGCTAAGACCATCTCAAAACAATCTGAAAAATGCTAAAAGGTACCTTCTCTGTGGAATAATCTGCAATGTCTAAAATCCTAAAATCCTAAAATCCTAAAATCCTAAAATCCTAAAATCAAAAATCAAAAAA	g dg	· •	QY 1070 TGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTG 1129 Db 781 TGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTG 840	D D
1833	090 CAGCCCAGAAAGGTGATTCTTCTCTTTACCATTTCTGGGGACTTTAGTCTTAATTAGGTA 1	D Qy		1010 c	D D
2089	030 TAGATGAAATAGAAGTTCAGGGTCCCTCACTCTAGTCACTAAAGAAGGATTTTACTCCCC	dq Qy		950 CTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGT 10	9 0 0
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1729	70 ACCCGAGGGGCGATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAATACGT	dd VQ		590 GGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTC 6	<u> 0</u>
1380	O CTTTGTTCTGTCCATCACACCACAACACGAGGCTTTGGCACTGATAGAACTCTATAATGC	ОУ		530 P	D O
1609 1320	O ACGAGTTGTCCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCAC 	Оу		470 TGACAGCTACAGTTCAGCTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCCG 52	
1549 1260	1490 GGAGCTGACGTGGGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAA 15	Qy		410 CAAATTCCCCACCAAAACTGGCCGAAGATCTTTTTTCTCGCTCG	<u>, o</u>
1489 1200		Qy		350 CACCGTCACCAAGGCGCCCAAGAAGCAAATCCAGTTTGCTGATGACATGCAGGAGTTCAC 4	<u>, e d</u>
1429 1140		Qу	,	290 CGGGGAGAAGCAGCAGGAGAAGCAGGAGAACGCCGAGAAAGTACTCCTTCATGGC 349	<u> </u>
1369		Qy	·•	Query Match 83.0%; Score 2126.8; DB 20; Length 3616; Best Local Similarity 97.4%; Pred. No. 0; Matches 2214; Conservative 0; Mismatches 32; Indels 28; Gaps 4	
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The invention relates to isolated polynucleotide (I) and CC polypeptide (II) sequences. (I) is useful as hybridisation probes, CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome CC and gene mapping, and in recombinant production of (II). The CC for identifying expressed genes. (I) is useful in gene therapy techniques CC for identifying expressed genes. (I) is useful in gene therapy techniques CC (II). (II) is useful for generating antibodies against it, detecting or CC quantitating a polypeptide in tissue, as molecular weight markers and as a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating CC disorders involving aberrant protein expression or biological activity. The polypeptide and polynucleotide sequences have applications in CC diagnostics, gene mapping, identification of mutations CC responsible for genetic disorders or other traits to assess biodiversity and to produce other types of data and products dependent on DNA and CC amino acid sequences: AAS64197-AAS94564 represent novel human CC diagnostic coding sequences of the invention.

CC Note: The sequence data for this patent did not appear in the printed content of the pulpo, int reminished and references.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess
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food supplement; medical imaging; diagnostic; genetic disorder; ss
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                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID No 12020; 103pp; English
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23-AUG-2000; 2000US-0649167.
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                                                                                                     1046 GCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAA
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ACAGAAATTTGACAACCTCTACTGTTGCCGTGAATCAATTCTTGATGGACTTAAAAGGAC
                                                                  ACTGTCCAAAGCTGGGAAGCTGTGTGTGTCCAGCCATGAATGTCAATGACTCAGTCACCAA
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73.8%;
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                                                                                                         s-adenosyl-5-homocysteine hydrolase; SAHH; human;
treatment; infection; cancer; autoimmune disease;
gene mapping; antisense; therapy; antagonist; imm
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           17-JUL-1997;
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                                                                                        Homo
                                                                                                                                                   Human SAHH DNA
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                              17-JUL-1997;
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                                                                                       sapiens
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(leukaemia, lymphoma or solid tumours), and many autoimmune diseases (e.g. acquired immune deficiency syndrome, allergy, asthma, disabetes melitus, multiple sclerosis etc). All these conditions may be treated by expressing antisense sequences, triplex-forming agents or ribozymes directed against the nucleic acid. The nucleic acid and its fragments can be used as probes or primers for detecting and quantifying gene expression, for diagnosis or monitoring of disease, to identify genetic variations, mutations or polymorphisms, in gene mapping and as antisense therapeutics. Antibodies are used directly as antagonists, indirectly to deliver active agents to SAHH-expressing cells, to diagnose and monitor diseases in standard immunoassays, in competitive drug screens and to isolate the protein from natural sources.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This sequence encodes a human S-adenosyl-5-homocysteine hydrolase (SAH protein can be used to generate specific antibodies and in dr screening to identify specific binding agents. Antagonists of the protein are used to treat or prevent a wide range of viral, bacterial, fungal, parasitic, protozoal or helminthic infections, many cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding human S-adenosyl-5-homocysteine hydrolase for production of recombinant enzyme, useful for diagnosis, treatment and prevention of cancers, infections and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5;
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(SAHH). drug

Sequence 2226 BP; 649 A; 455 C; 435 G; 675 T; 12 other;

Query Match Best Local s Matches 830 GCAAAATATCTGGGACTCAACAAAAATGGGCCATTCAAACCTAATTATTACAGATACTAA 830; Similarity Conservative 31.5%; Pred. 0; Mis Score 806.2; Mismatches No. 1.6e-198; DB 20; Indels Length 2 Gaps 1847 60 1787 120 2

TGGACCATACTACCAAGGACCAGTCCACCTGAACCACACACTCTAAAGAAATATTTTTTA TGGACCATACTACCAAGGACCAGTCCACCTGAACCACACTCTAAAGAAATATTTTTTA 1967 180

2027 240

TTTAGATGAAATAGAAGTTCAGGGTCCCTCACTCTAGTCACTAAAGAAGGATTTTACTCC

CCCAGCCCAGAAAGGTGATTCTTCTCTTTACCATTTCTGGGGACTTTAGTCTTAATTAGG TTTAGATGAAATAGAAGTTCAGGGTTCCTCACTCTAGTCACTAAAGAAGGATTTTACTCT

2147

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2087

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TACCTTATTAACAGGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAA TACCTTATTAACAGGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAA CCCAGCCCAGAAAGGTGATTCTT-TCTTTACCATTTCTGGGGACTTTAGTCTTAATTAGG 2207 479 419

TCGCCTTAAAAGAGCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAG 539 2267

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RESULT 7
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proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; prollferative disorder; wound; infactious disease; ss.
                                                                                                                                                                                                                                                                                  Claim 1; Page 917-918; 2338pp; English
                                                                                                                                                                                                                                                                                                                                                Prostate cancer associated gene sequences, cancer antigens, useful for treatment, predisorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-)
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                                                                                                                                                                                                                                          AAF15566 to AAF16505 encode the human prostate cancer associated
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLG1847-ABL30511), expressed DNA sequences (ABLG1847-ABL30511), and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; SEQ ID NO 5561; 21pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
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    Drosophila; developmental biology; cell signalling; insecticide;
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                                         Drosophila melanogaster genomic polynucleotide SEQ ID NO 40834.
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Best Local Similarity
Matches 937; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 40834; 21pp + Sequence Listing; English
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11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ABB57737-ABB72072).
The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                  ATGAAGTAGCTGCAGCACCACCTGAGGCTGGAGGTGCAGTGTTCCGCTTGGAAGGGCGAGT
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17-MAY-2002

(first entry)

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                                                                                                                                                                                                                                                                                                                                                                                     CC ABL67934. (III) encoding (II) having a sequence (S2), a T cell
cc population of (II), or antigen presenting cells that express (II).
cc (I) has cytostatic activity. An oligonuclectide (IV) that hybridises to
cc (S1) can be used for detecting ovarian cancer in a patient's biological
cc contacting a biological sample from a patient with (IV), detecting the
cc contacting a biological sample from a patient with (IV), detecting the
cc amount of polynuclectide hybridising to (IV) and comparing the amount to
cc a predetermined cutoff value and thereby detecting ovarian cancer in the
cc entient, where the amount of polynuclectide hybridising to (IV) is
cd detected preferably by polymerase chain reaction (PCR). (I) comprising
cc (III) and/or (II) is useful for stimulating and/or expanding T cells
cc with (III) or (III) is useful in design and preparation of
cc with (III) or (III) is useful in design and preparation of
cc with (III) or (III); and tumour cells; and to isolate a full length gene from a
cutable library e.g., a tumour CDNA library using well known
                                                                                                                                                                                                                                                                       Best Loc
Matches
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polynucleotide (III) having a cDNA sequence polypeptide encoded by a polynucleotide (III) having a cDNA sequence in ABL77023 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing
                                                                                                                                                                                                                                      1322 GGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAA 1381
                                                                                                                                                                                                                                                                                                                                       Sequence 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 1; SEQ ID 2023; 489pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human ovarian cancer related cDNA clone SEQ ID NO: 2023
                                 1502
 181
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                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                      _
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         present invention describes a composition (I) comprising: carriers
                                                                                                                                   GGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAA
GGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGAT-GNAAACGAGTTGTCCT
                               GGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCT
                                                                   TATGGGCCACTCCAACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTG
                                                                                                   TATEGECCACTCCAACACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTG
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                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                           BP;
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                                                                                                                                                                                                                                                                                                                                            159 A; 136
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                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                         Score 492.4; DB 24; Length Pred. No. 2e-117;
                                                                                                                                                                                                                                                                                                                                            128 G;
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                                                                                                                    genes from Drosophila interactions -
                                                                                                    Claim 1; SEQ ID NO 5558; 21pp + Sequence Listing; English
                                                                                                                                       New isolated nucleic
                                                                                                                                                                                 Venter JC,
                                                                                                                                                                                                                    23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                WO200171042-A2
                                                                                                                                                                                                                                                                                                 Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                  pharmaceutical;
                                                                                                                                                                                                                                                                                                                          Drosophila;
                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster expressed polynucleotide SEQ ID NO
                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002
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                                                                                                                                                        2001-656860/75.
DB; ABB59589.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; cDNA; 4406
                                                                                                                                                                                 Adams M,
                                                                                                                                                                                                                                                                                                                         developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                   2000US-191637P
2000US-0614150
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                                                                                                                                                                                                                                                                                                                  gene;
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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins

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The sequence data for this patent did not form specification, but was obtained in electronic at ftp.wipo.int/pub/published_pct_sequences.

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TGTACTTGCTTCCTAAGAAAATGGATGAATÄCGTTGCCAGCTTGCATCTGCGTCATTTG
                                      CACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGGCGATACAAGCAGGATG
                                                                                                                       GTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCATCACAGCCACAA 1635
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Query Match Best Local Sim Matches 422;

Similarity

100.0%; 16.5%;

Score 422; DB 23; Pred. No. 3.5e-99;

Length Indels

504; 0;

Conservative

0,

Mismatches

0

Gaps

0

Sequence

504

B₽;

117 as a

A; 150 C;

116 G; 121 T; 0 other;

also useful

pharmacodyanamic

ç

pharmacogenomic

(e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a

prostate cancer

in a patient;

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RESULT 12
ABV44141/c
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                                                                                                           specification or its complement. (I) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer.
                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV44141
                                                                                                                                                                                                                              Claim 1; Page
                                                                                                                                                                                                                                                             Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                    Schlegel
                                                                                                                                                                                                                                                                                                                                                                                                              09-JUN-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                          16-MAR-2000;
25-MAY-2000;
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2000US-207454P.
2000US-211314P.
2000US-211907P.
2000US-255281P.
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                                                                                                                                                                                                                                                        presence of prostate cancer, stage of prostate
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 The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila;
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   pharmaceutical;
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                                                                                      Claim 1; SEQ ID NO 40831; 21pp + Sequence Listing; English
                                                                                                                                          New isolated nucleic a
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The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
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                                                                                                                                                                                                                                                               Human; gene expression product; diagnosis; tumoùr; colorectal adenocarcinoma; cell line SW480; cell pr cytostatic; sarcoma; breast cancer; neoplasia; dysp
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                                                                    Endege WO, Carroll E,
                                                                                                                         10-วบพ- มูล 98;
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                                                                                                         (FARB ) BAYER
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                                                                                                                                                                                                                                                   nyperplasia;
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Novel nucleic acids, used to develop products for the diagnosis and treatment of disorders involving unwanted cell proliferation,

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                                                         diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiviral; antidiabetic; antiasthmatic; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; haematopoietic cell disorder; autoimmune disorder; praft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the human colorectal adenocarcinoma (colon cancer) cell line SW480. The CDNA clones can be used to generate antisense oligonuclectides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The CDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia dysplasia or hyperplasia.
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              Homo sapiens
                                                neurological
                                                                                                                                                                                                             Human; cancer associated gene; cancer antigen; detection; cancer;
                                                                                                                                                                                                                                                Human cancer associated gene sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAZ79917 to AA280766 represent double stranded cDNA clones isolated
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                                                                                                                                                                                                                                                                                                                                                           standard;
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                                                 disease;
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99.5%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antidiabetic; antiasthmatic; antirheumatic; antiarthritic;
antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the
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Search completed: April 20, Job time: 578 secs 2003, 14:39:52

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SOURCE ORGANISM REFERENCE AUTHORS TITLE	RESULT 1 AX029176 LOCUS DEFINITION ACCESSION VERSION KEYWORDS		41 42 44 45	c 38 40	C 3354 3654	3 2 2 1 d	322 29 29	0 0 2 0 5 5	c 222 233	c 19		o 14	11 12 13		തെ	ω ω Ν μ	Result
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//LIANS 1841001-"RGOYGARSCCFWFSCGHRRCPAALGCRTDKAWATAPOKPTQLDA 
/LIANS 1841001-"RGOYGARSCCFWFSCGGGGSAAGRAGGMSMPDAMPLPOYGEELKQ 
AKELEDAEKYSFMATYTKAPKKOLOPADDMOETKFPTRTGRRSLSRSISOSSTOSYS 
SAASYTDSSDDEVSPREKOOTNSKGSSMFCVKNIKQAEFGRREIEIAEQDMSALISLR 
KRAGGEKPLAGAKIYGCTHITAQTAVLLETLCALGAQCKWSACNIYSTONUFAKLISLR 
KRAGGEKPLAGAKIYGCTHITAQTAVLLETLCALGAQCKWSACNIYSTONUFAKLIRG 
AGYAVFAWKCESEDDFWWCLDRCYNNDGWQANNILDDGGDLTHWYYKKYDNVFKKIRG 
IVEESYTGVHRLYQLSKAGKLCVPAMNVDDSVTKQKFDNLYCCRESILDGLKRTTDVM 
FGGKQVVVCGYGEVGKGCCAALKALGALVYITEIDPICALQACKDGFRVVKLHEVIRQ 
VDVVITCTGNKNVYTREHLDRKNSCIVCNMGHSNTEIDVTSLRTPELTWERVRSQVD 
HVIWPDGKRYVLLAEGRLLNLSCSTVPTFVLSITATTQALALIELIYNAPEGRYKQDVY 
LLPKKMDEVYASLHLPSFDAHLTELTDDQAKKLGLAKNGPFKPNYYRY"

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GATACAAGCAGGATGTGCTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGCTTGC
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      Eukaryota; Metazoa; Chordata; Mammalla; Eutherla; Primates; 1 (bases 1 to 2677)
Dekker, J.W., Budhia, S., Angel,
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         Angel, N.Z.,
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         Cooper, B.J.,
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                            Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                              1 GCCGCGGCAGGTCGGAGCTCGGAGCTGCTGCTCTGGTTCTCTTGTGGCCACCGTCGCT
                                                                                                                                                                                                                                                                                                       GTCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCAGAAGCCGA
TGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGGCCACCGTCACCA
                                                         GGGCAGGCGGGCGGCCCAGAGGGGGGAAAGAGGCGGGGGCGGGCGGGTCAGCCGCTGGCC
                                                                                                                                                                                                                          CGCAGCTCGACGCAGGGGCCGGCAGGAGGGTGGGCGATCGCGTGTCGGAGGGCGCCGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Identification of an S-adenosylhomocysteine hydrolase-like transcript induced during dendritic cell differentiation Immunogenetics 53 (12), 993-1001 (2002)
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Hart, D.N.J. and Kato,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="S-adenosylhomocysteine hydrolase-like protein"
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/db_xref="G1:16588687"
/db_xref="G1:16588687"
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LIETLCALGAQCRWSACNIYSTQNEVAKALAEAGVAVFAMKGESEDDFWAGIDTGVNM
DGWQANMILDDGGDLTHWYKKXYPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPAM
NVNDSYTKQKFDNLYCCRESILDGLKRTTDVMFGGKQVVCGYGEVGKGCCAALKALG
AIVYITEIDETCALQACMDGFRVVKLKEVIRQVDVYTGTGNKNVVTREBLLDKAKALG
AIVYITEIDETCALQACMDGFRVVKLKEVIRQVDHVIWPDGKRVVLLAEGRLLNLSCSTV
PTFYLSITATTQALALIELYNAPEGRYKQDDVILLFKKMDEYVASLHLPSFDAHLIELT
PTFYLSITATTQALALIELYNAPEGRYKQDVYLLFKKMDEYVASLHLPSFDAHLIELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note-"DCAL; dendritic cell expressed AHCY-like protein; expressed in dendritic cells in blood, Langerhans cells and dermal dendritic cells; mRNA increased during monocyte differentiation to monocyte-derived dendritic cells in the presence of GM-CSF and IL-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDQAKYLGLNKNGPFKPNYYRY"
648 c 708 g 6
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/db_xref="taxon:9606"
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	ATATGGGCCACTCCAACACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGT 15		1 GGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAA 1380 	1 TTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGGATGG	1 TGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTGCTG	ш ш			61 GGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAAGCCATTGTGGAAGAGAGCG 1020 	1 TGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACT 960 	41 CAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGGTGTATTGACCGCTGTG 900	81 CTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGG	21 CCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGGCTCAGTGCCGCTGGTCTG 780	51 GTGCTCAGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACACACATCACAG 720 	01 GACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAAC 660 	41 AAACCAACTCCAAGGGCAGCAATTTCTGTGTGAAGAACATCAAGCAGGCAG	81 GTTCAGCTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGC 540 	21 CCAAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACA 480	61 AGGCGCCCAAGAAGCAAATCCAGTTTGCTGATGACATGCAGGAGTTCACCAAATTCCCCA 420
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	ργ	Qy	Db Qy	og Db	Db dg	gg dg	Qy db	Qy db	dd Vy	dd Qy	Db Qy	Db Qy	Db Db	Qy Db	Qy db	dg VQ	dd Qy	gb Qy	da da
-	2521 TCTAGGATTTATTTCTGTTGTCCAAAAAAAAAAAAAAAA	2461 GACTTGCTCATTTTTCGAGTTTTTAACTAGACTACACTCTATTTGAGTTTAATTTTGTCC 2520	2401 CTTGTTAAGATCAGGAGGCCCACTTGGATTTATAGTATAGCCCTTCCTCCACTCCACCAC 2460	AGCCCTGTT	2281 ACCTACCCGGCAGGTAGGTTAGATGTGGGTGGTGCATGTTAATTTCCCTTAGAAGTTCCA 2340	2221 GCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAGAAGCAGGGATGGT 2280	2161 GGAAATGCTAAGGTACCTTCTCTGTGGAAGATCTGCAATGTCTAAATGCCCTTAAAAGA 2220	2101 GGTGATTCTTCTGTTTACCATTTCTGGGGACTTTAGTCTTAATTAGGTACCTTATTAACA 2½6	2041 GAAGTTCAGGGTCCCTCACTCTAGTCACTAAAGAAGGATTTTACTCCCCCAGCCCAGAAA 2100	ъ <u>р</u>		1861 CAAGGACCAGTCCACCTGAACCACACTCTAAAGAAATATTTTTTAAGATAACTTTTAT 1920	5 1	1741 ATCTGCCATCATTTGATGCCCACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGG 1800	1681 GATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGCTTGC 1740	621 CCATCACAC 735 CCATCACAC	61 75	01 GGGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCC 	
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2492; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Meb site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mod@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission
Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2552 bp mRNA linear
Homo sapiens, S-adenosylhomocysteine hydrolase-like
MGC:21453 IMAGE:3450568, mRNA, complete cds.
BC016942
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Tissue Procurement: ATCC
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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YSSAASYTDSSDEYSPREKQOTNSKGSSNFCVKNIKQAEFGRREIEIAEODMSALIS
LRKRAQGEKPLAGAK VECTHITAQTAVLIETICALGACKGEWSACNIY STQNEVAKAI
AEAGYAVTAWKGESEDLYGCTHITAQTAVLIETICALGACKGEDLTHWVYKKYPNVFKKI
RGIVEESVTGVHRLYQLSKAGKLCVPAMMVNDSVTKQKFDNLYCCRESILDGLKRTTD
VMFGGKQVVVCGYGEVGKGCCAALKALGAIVYITEIDPICALQACMDGFRVVKLNEVI
                                                                                                                            VYLLPKKMDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGPFKPNYYRY
600 c 671 g 637 t
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/db_xref="LocusID:10768"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="placenta, choriocarcinoma"
/clone_lib="NIH_MGC_10"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                        'db_xref="GI:16877387"
                                                                                                                                                                                                                                                                                                                          /product="S-adenosylhomocysteine hydrolase-like
/protein_id="AAH16942.1"
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TCATTTTTCGAGTTTTTAACTAGACTACACTCTATT
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Homo sapiens.
Eukaryota; Metazoa; C
Mammalla; Eutherla; P
1 (bases 1 to 2526)
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Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Genome Sequence Centre,
BC Canada
Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LiML at: http://image.linl.gov/series: IRAL Plate: 22 Row: h Column: 21

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                         Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Histao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.
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Submitted (10-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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MGC:15558 IMAGE:3139729, mRNA, complete
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/SSAASYTDSSDDEVSPREKQQTNSKGSSNECVKNIKQAEFGRREIEIAEQDMSALIS
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AEAGVAVFAWKGESEDDFWWCIDRCVNMDGWQANMILDDGGDLTHWVYKKYPNVFKKI
RGIVEESVTGVHRLYQLSKAGKLCVPAANNVNDSVTKQKFDNLYCCRESILDGLKRTTD
VMFGGKQVVVCGYGEVGKGCCAALKALGAIVITIEIDPTCALQACMDFRVVKLEVI
RQVDVVITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLRTPELTWERVRSQ
VDHYUMPDGKRVVLLAEGRLLNLSCSTVPTFVLSITATTQALALIELYNAPGGRYKQD
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                                                                                                                                                                                                   Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hul
                                                             DNA Sequencing by: Baylor 
Sequencing Center
                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Contact: MGC help desk
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GTTCAGCTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGC
                             TGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGGCCACCGTCACCA
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                                                                                                                            AGGCGCCCAAGAAGCAAATCCAGTTTGCTGATGACATGCAGGAGTTCACCAAATTCCCCA
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                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.series: IRAK Plate: 13 Row: b Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA g1: 572
Location/Qualifiers
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Muzny, D.M., Gibbs, R.
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YSSAASYTDSSDDEVSPREKQQTNSKGSSNFCVKNIKQAEFGREIIFAEQDMSALIS
LRKRAGGERFLAGAKIVGGTHITAQTAVLIETLCALIAQCEMSACINIYSTQNEVAAAL
AEAGVAVFAWKGESEDDFWWCIDRCVNNDGWQANNILDDGGDLTHWYYKKY PAVFKKI
RGIVEESVTGVHRLYQLSKACKLCVPAMNVNDSVTKQKDDNLYCCRESILDGLKRTTD
VMFGGKQVVVCCGYGEVGKGCCAALKALGYIVTITEIDPICALQACNDGFRVYKLNEVI
RQVDVVTTCTGNKNVVTREHLDRMKNSCIVCNNGHSNTEIDVTSLKTPELTWWERVRSQ
VDHVIWPDGKRVVLLAEGRLLNLSCSTVPTFVLSITATTQALALIELYNAPEGRYKQD
VYLLPKKMDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGPFKPNYYRY"
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/protein_id="AAH10681.1"
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/clone_lib="NIH_MGC_65"
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/clone="McC.con"
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/db_xref="LocusID:10768"
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/db_xref="GI:14715038"
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HSU82761 Pomo sapiens S-adenosyl h mRNA, complete cds. U82761 U82761.1 GI:2852124 Homo sapiens Homo sapiens Eukaryota; Metazoa; Chord		CAGGTA	AAGGTAC	GTTCTT	AGTTCTO	TCCACCI 	ATTTGAJ	CACAACA CACAACA GGATGTC
2258 lete cds. 31:2852124 Metazoa; Chordata;	 GGCCCAC GAGTTTT GAGTTTTT	GGTTAGA TAAAGGT	CTTCTCT CTGAAAT CTGAAAT CTGAAAT	CACTCTA ACCATTT ACCATTT ACCATTT	GCAGACC	TGAACCA GAACCA 	rgcccac rgcccac gccattc	ACAGGCT ACAGGCT ACAGGCT STACTTG
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mol			ATGCTAGGTAGGTTAGATGTGGGTGGGTGGGTGGATGTTTAGATGCCTTAAAAAGAAGTTCTAAAAAGAAGTAGCCTTAAAAAGAAGAAGGAAG	TICAGGGTTCCTCACTCTAGTCACTAAAGAAGGATTTTACTCTCCCAGCCCAGAAA ATTCTTCTCTTTAACATTTCTGGGGACTTTAGTCTTAATTAGGTACCTTATTAACA	TATICCAAGITCTGCAGACCACACAGGAACITGCTTCATGGCTCTTTAGATGAAATA	GACCAGTCCACCTGAACCACACTCTAAAGAAATATTTTTTAAGATAACTTTTA†	ATCTGCCATCATTGATGCCCACCTTACAGAGGTGACAAGTGACCAAGCAAAATATCTGG	CACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCGAGGGGG
PRI 17-DEC-20.og (XPVkona)	CCA 2481	TGG 2400	AGA 2241 GGT 2280 1 2301 CCA 2340	AAA 2122 ACA 2160 	ATA 2040 111 ATA 2062 AAA 2100	TAT 1920 TAT 1942 TATC 1980		
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                                                            ACAGTTCAGCTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGC
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1 (bases 1 to 2258)

Cleaver, J.E., Afzal, V., Feeney, L., McDowell, M., Sadinski, W., Volpe, J.P.G., Busch, D.B., Coleman, D.M., Ziffer, D.W., Yu, Y., Nagasawa, H. and Little, J.B.
Increased ultraviolet sana (1)
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2 (bases 1 to 2258)
3 (olpe, J.P.G., McDowell, M., Jostes, R.F., Afzal, V., Volpe, J.P.G., McDowell, M., Jostes, R.F., Afzal, V., Trask, B.J., Legerski, R. and Cleaver, J.E.
5 (complementation of chromosomal instability in the pigmentosum variant by a gene on human chromosome pigmentosum variant by a gene on human chromosome pigmentosum variant by a gene on human chromosome
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Volpe, J.P.G., McDowell, M. and Cleaver, J.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (19-DEC-1996) Dermatology, 0750, San Francisco, CA 94143, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Increased ultraviolet sensitivity and chromosomal instability related to P53 function in the xeroderma pigmentosum variant Cancer Res. 59 (5), 1102-1108 (1999)
                                                                                                                                                                                                                                                                                                                                    Similarity
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/tsaaasytdssddevsprekQqtnskGssnecvknikQaefgrreleiaeqdmsalis 

LRKRAQGEKFLAGAKIVGCTHLTAQTAYLIETLCALGAQCRWSACHIYSTQNEVAAAL 

AEAGVAVFAMKGESEDDFFWGLIDRCVNDGWQANMILDGGDLTHWYKKYPNVFKKI 

RGIVEESVTGVHLLYQLSKAGKLCVPAANVNDSVTKQKFONLYCCRESILDGLKRTTD 

VMFGGKQVVVCGIGEVGKGCCAALKALGAIVYITEIDFICALQACMDGFRVVKLNEVI 

RQYDVVITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLAFPELTWERVRSQ 

VDHVIMPDGKRVVLLAEGRILUNLSCSTVPTFVLSITATTQALALIELYNAPEGRYKQD 

VDHVIMPDGKRVVLLAEGRILUNLSCSTVPTFVLSITATTQALALIELYNAPEGRYKQD 

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/protein_1d="AAC01960.1"
/db_xref="GI:2852125"
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                  TGTCCATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGG
                                TGTCCATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGG
                                                                             TCCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCCACCTTTGTTC
                                                                                               TCCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTC
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sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp564A152) is available at the RZPD in Berlin Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 1405 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
                                                               Submitted (15-MAY-1999) MIPS, Am Klopferspitz 18a, D-82152 MARTINSTIED, GERWANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
                                                                                                                            Eukaryota, Metazoa; Chordata; Craniata; Vertebrata, Mammalia; Eutheria; Primates; Catarrhini; Hominidae
Mammelia; Eutheria; Primates; Catarrhini; Hominidae
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Wambutt,R., Heubner,D., Mewes,H.W., Gassenhuber,J.
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partial cds.
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Best Local Similarity
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                 CTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTI
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illarity 99.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product-"hypothetical protein"
/protein_id="CAB4323.1"
/protein_id="CAB4323.1"
/db_xref="GI:484204"
/translation="GLLTVELDSSCVCYILLLEHRGGSRRGKICAEISQPALPLPQE
/translation="GLLTVELDSSCVCYILLLERRLYSAQGNGRSDMRWHUMIOLWPELDSLE
TQAPSGESENLRNLAQGRRAESSQNILSLRRLYSAQGNGRSDMRWHUMIOLWPELDSLE
ISCFLQIQFADDMQEFTKFPTKTGRRSLSRS ISQSSTDSYSSAASYTDSSDDEVSPRE
KQQTNSKGSSNFCVKNIKQAEEGRREIEIAEQDMSALISLEKRAQGEKPLAGAKIVGC
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AGKLCVPAMNVNDSYTKQKFUNLYCCRESILDGLKRTTDVMFGGKQVVVCGYGEVGKG
CCAALKALGAIVYITEIDPIGALGHEVELNEVIDDVYITCTGGKKNVVTRE
CLALKALGAIVYITCHDFIGALGHEVELTWERVRSQVDHYIWPDGKRVVLLAEGR
HLDRWKNSCIYCNGHSNTEIDVTSLRTPELTWERVRSQVDHYIWPDGKRVVLLAEGR
LLNLSCSTVPTFVLSITATTQALALIELYNAPBGRYKQDVYLLPKKMDEYVASLHLPS
FDAHLTELTDDQAKYLGLNKNGPFKPNYYRY"
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/clone_lib="564 (synonym: hfbr2). Vector pAMP1;
x1-2blue; sites NotI + SalI"
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/clone="DKFZp564A1523"
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/db_xref="taxon:9606"
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	1873 1822	CTACCAAGGACCAGTCC	1814
	81	GATGCCCACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGGGACTCAACAAAA 	0 5
	1753 1702	TGTGTACTTGCTTACTAAGAAAATGGATGAATACGTTGCCAGCTTGCCATCTGCCATCATT 	1694 1643
	1693 1642	AACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGCGATACAAGCAGGA	1634 1583
	1633 1582	TCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCATCACAGCCAC	1574 1523
	1573 1522	TTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCTCCTGGCAGAGGG	1514 1463
	1513 1462	CAACACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCGAGTACG	
	1453 1402	GACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTC 	1394 1343
	1393 1342	AAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATGTAGT	
	1333 1282	CGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGGATGG	1274 1223
	1273 1222	TGAGGTAGGCAAGGGCTGCTGTGCTGCTCTCAAAGCTCTTGGAGCAATTGTCTACATTAC	1214 1163
	1213 1162	CCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGT	1154 1103
	1153 1102	TTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTGGATGG	1094
	1093	CAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACGTCAATGA	1034 983
	1033 982	GTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGAAGAGAGAG	974 923
	973 922	GTGGCAGGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACTGGGTTTATAAGAA 	914 863
•	913 862	GAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTGTGAACATGGATGG	854 803

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REFERENCE AUTHORS TITLE JOURNAL MEDLINE PUBMED REFERENCE AUTHORS TITLE JOURNAL SOUTO	RESULT 8 AF035319 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM REFERENCE AUTHORS TITLE JOURNAL MEDLINE	Qy 2474 Db 2422	Qy 2414 Db 2362	Qy 2354 bb 2302	Qy 2294 Db 2242	Qy 2234 Db 2182	Qy 2174 Db 2122	Qy 2114 Db 2062	QУ 2054 . Db 2003	Qy 1994 Db 1943	Db 1883
ED 8619474 2 (bases 1 to 1369) 2 (bases 1 to 1369) Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A. Large-scale concatenation cDNA sequencing AL Genome Res. 7 (4), 353-358 (1997) NE 97264341 ED 9110174 ED 9110174 ED 9110174 ED 9110174 ED 9110174 Chases 1 to 1369) XI Sarginson,J. and Gibbs,R.A. Direct Submission AL Submitted (20-NOV-1997) Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza S930, Houston, TX 77030, College of Medicine, One Baylor Plaza S930, Houston, TX 77030, College of Medicine, One Baylor Plaza S930, Houston, TX 77030, Location/Qualifiers 1. 1369 //db_xref="taxon:9806"	AF035319 AF1035319 AF10	74 TICGAGITITAACIAGACIACACICIAIT 2503 	4 GGAGGCCCACTTGGATTTATAGTATAGCCCTTCCTCCACTCCCACCAGACTTGCTCATTT 2473	54 GCGTAAAGGTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGGCTTGTTAAGATCA 2413 	94 GTAGGTTAGATGTGGGTGGTGCATGTTAATTTCCCTTAGAAGTTCCAAGCCCTGTTTCCT 2353	34 CTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAGAAGCAGGGATGGTACCCTACCCGGCAG 2293	74 TACCTTCTCTGTGGAACAATCTGCAATGTCTAAATCGCCTTAAAAGAGCCCATTTCTTAG 2233 	14 TITACCATITCTGGGGACTITAGTCTTAATTAGGTACCTTATTAACAGGAAATGCTAAGG 2173 	54 CCTCACTCTAGTCACTAAAGAAGGATTTTACTCCCCCAGCCCAGAAAGGTGATTCTTCTC 2113 	94 TCTGCAGACCACAGAGAACTTGCTTCATGGCTCTTTAGATGAAATAGAAGTTCAGGGTC 2053 	33 CTTTCCTCTTGATTTTTTTCCTATAATTTCATTCTTGTTTTTCATCTATAATCCAAGT 1942
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                                         GACTCAACAAAATGGGCCATTCAAACCTAATTATTACAGATACTAATGGACCATACTAC
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VVKLNEVIRQVDVVITCTGNKNVVTREHLDRKKNSCIVCMMGHSNTEIDVTSLRTPEL
TWEBVRSQVDHVIWPDGKRVVLLAEGRLLNLSCSTVPTFVLSITATTGALALIELIYNA
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/note="This clone is similar to Drosophila renoded by GenBank Accession Number L07835.
Consortium clone ID number is 23931"
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/db_xref="GI:2661083"
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	REMAR COMMENT	REFE AU TI JO	RESULT 9 BC003631 LOCUS DEFINITIO ACCESSION VERSION KEYWORDS SOURCE ORGANI	g 97	ρ γ	рь Оу	gg VQ	g qq	D QY	g Qy	B 84	Dy Dy	ОУ
	MENT MENT	SFERENCE AUTHORS TITLE JOURNAL	RESULT 9 BC003631 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE ORGANISM	2461 1270	2401 1210	2341 1150	2281 1090	2221 1030	2161 970	2101 911	2041 851	1981 791	1921 731
	gov Rubin Laboratory The I.M.A.G.E. Con Lute for Systems B1 Lology.org fology.org Anuradha Madan	Mammalia; Eutheria; Primates; 1 (bases 1 to 1323) Strausberg,R. Direct Submission Submitted (26-FEB-2001) Nation Gene Collection (MGC), Cancer Institute, 31 Center Drive, Ro	BC003631 Homo sapiens, Similar to S-adenosylhomocysteine hydro clone IMAGE:3010755, mRNA, partial cds. BC003631.1 GI:13177702 Homo sapiens. Homo sapiens. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E	GACTTGCTCATTTTTGGAGTTTTTAACTAGACTACACTCTATT 2503	CTTGTTAAGATCAGGAGGCCCACTTGGATTATAGTATAG	AGCCCTGTTTCCTGCGTAAAGGTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGG 2400	ACCTACCCGGCAGGTAGGTTAGATGTGGGTGGTGCATGTTAATTTCCCTTAGAAGTTCCA 2340	GCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAGAAAGCAGGGATGGT 2280 	GGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAAATGCCCTTAAAAGA 2220 	GGTGATTCTTCTCTTTACCATTTCTGGGGACTTTAGTCTTAATTAGGTACCTTATTAACA 2160 	GAAGTTCAGGGTCCCTCACTCTAGTCACTAAAGAAGGATTTTACTCCCCCAGCCCAGAAA 2100	TCATTATCCAAGITCTGCAGACCACACAGGAACTTGCTTCATGGCTCTTTAGATGAAATA 2040	THICTTCHACTCCTTTCCTCTGATTTTTTCCTATAATTCATCTTGTTTTTTCATC 1980

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                                 AATGGACCATACTACCAAGGACCAGTCCACCTGAACCACACACTCTAAAGAAATATTTTT
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CTGNKNYVTREHLDRMKNSCTVCNMGHSNTEIDVTSLRTPEITWERVRSQVDHYIWPD
GKRVVLLABGRLLNLSCSTVPTFVLSITATTQALALIELYNAPBGRYKQDVYLLPKKM
DEYVASLHLPSFDAHLTELTDDQAKYLGINKNGPFKPNYYRY"
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/db_xref="GI:13177703"
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'closue_type="Muscle, rhabdomyosarcoma"
'clone_lib="NIH_MGC_17"
'lab_host="DH10B-R"
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78	ery st tch		THORS	VERSION KEYWORDS SOURCE ORGANIS	ULT 10 68569 US INITIO	2446 1209	2386 1149	1089	2266 1029	2206 969	2146 909	2086 850	2026 790	1966 730	670
78	ery Match 21.6%; Score 553; DB 6; Length 2226; st Local Similarity 99.6%; Pred. No. 7.7e-311; tches 773; Conservative 0; Mismatches 2; Indels 1; 1728 GTTGCCAGCTTGCATCATCATTGATGCCCACCTTACAGAGCTGACAGATGACCA	Source 12226 source 12226 count 649 a 455 c 4	CE 1 (bases 1 to 2226) RS Hillman, J.L., Corley, N.C., Lal, P. and Shah, P. Polynucleotides encoding human S-adenosyl-5-homocysteine derived from bladder derived from bladder 29-DEC-1998; AL Patent: US 5854023-A 2 29-DEC-1998;	·	T 10 569 AR068569 2226 bp DNA linear PAT 2 ITION Sequence 2 from patent US 5854023. SION AR068569	446 CCTCCACTCCACCAGACTTGCTCATTTTTCGAGTTTTTAACTAGACTACACTCTATT	μ ω	ο ω	266 AGAAGCAGGGATGGTACCTACCCGGCAGGTAGGTTAGATGTGGGTGG	206 AATCGCCTTAAAAGAGCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACTTCTTCA 	9 14	8 0	02 79	ωσ	7
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                                                                                                                       Detection of analytes using attenuated enzymes Patent: WO 0102600-A 3 11-JAN-2001; GENERAL ATOMICS (US)
                                                                                                                                                                                                                                                     AX069339 2226 bp
Sequence 3 from Patent W00102600.
AX069339 GI:12579202
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1 (bases 1 to 2226)
                                                                                                                                                                                                                     Homo sapiens
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                                /note-"Polynucleotide encoding human
S-adenosyl-5-homocysteine hydrolase (SAHH) derived
bladder; n-a, c, g, or t."
455 c 435 g 675 t 12 others
                                                                                        /organism="Homo sapiens"
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lla; EUCHERIA; FILMATES; CATATIAINI; HOMINIDAE; HOMASES 1 to 81378) n,S. t Submission t Submission tted (16-AUG-2002) Wellcome Trust Sanger Institute, idgeshire, CB10 ISA, UK. E-mail enquiries:	AL//2411.1 G1:21534613 HTG. human. human. Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi	sequence them cross service on caroline to sequence the sequence of caroline to sequence the sequence of the s	AL772411 81378 bp DNA linear PRI 1	TCCACTCCACAGACTTGCTCATTTTTCGAGTTTTTAACTAGACTACACTCTATT 775	TCCACTCCCACCAGACTTGCTCATTTTTCGAGTTTTTTAACTAGACTACACTCTATT 2503	vo a	ى د	CTTAGAAGTTCCAAGCCCTGTTTCCTGCGTAAAGGTGGTATGTCCAGTTCAGAGATGTGT 2387	AAGCAGGGATGGTACCTACCCCGCCAGGTAGGTTAGATGTGGGTGG	AAGCAGGGATGGTACCCTACCCGGCAGGTAGGTTAGATGTGGGTGG	TCGCCTTAAAAGAGCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAG 539	TCGCCTTAAAAGAGCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAG 2267	TACCTTATTAACAGGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAA 479		CCCAGCCCAGAAAGGTGATTCTTCTCTTTTACCATTTCTGGGGACTTTAGTCTTAATTAA	TTAGATGAAATAGAAGTTCAGGGTTCCTCACTC	TTTAGATGAAATAGAAGTTCAGGGTCCCTCACTCTAGTCACTAAAGAAGGATTTTACTCC 2087	TIGITITIZATORIC CATTATCCAAGITCTGCAGACACACACACAGGAACTTGCTTCATGGCTC 300	3 (19	TGGACCATACTACCAAGGACCAGTCCACCTGAACCACACTCTAAAGAAATATTTTTTÄ 180	TGGACCATACTACCAAGGACCAGTCCACCTGAACCACACTCTAAAGAAATATTTTTTA 1907	GCAAAATATCTGGGACTCAACAAAAATGGGCCATTCAAACCTAATTATTACAGATACTAA 120	GCAAAATATCTGGGACTCAACAAAAATGGGCCATTCAAACCTAATTATTACAGATACTAA 1847	GTTGCCAGCTTGCATCTGCCATCATTTGATGCCCACCTTACAGAGCTGACAGATGACCAA 1/8/ 	al Similarity 99.6%; Pred. No. 7.7e-311; 773; Conservative 0; Mismatches 2; Indels 1; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk On Aug 19, 2002 this sequence version replaced gi:13396588.
During sequence assembly data is compared from overlapping clones where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1 constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr1
http://www.sanger.ac.uk/HGP/Chr1
RP11-180N18 is from the library RPCI-11.1.constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Wellcome Trust Sanger Institute
Center code: SC
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Cambridge, MA 02141, USA
http://www-seq.wi.mit.edu
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database can be found at
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Contact: humquery@sanger.ac.uk
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/clone_1ib="RPCI-11.1"
17337 c 18556 g 23719
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/db_xref="taxon:9606"
/chromosome="1"
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Pred. No. 2.7e-248;
D; Mismatches 2;
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                                                                                              Web site: http://www.contact: humquery@sanger.ac.uk
Contact: humquery@sanger.ac.uk
Project Information
hal80N18
Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7815; 25% of reads
Sequencing vector: plasmid; L08752; 74% of reads
Chemistry: Dye-terminator ET-amersham; 21% of reads
Chemistry: Dye-terminator B1g Dye; 78% of reads
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo
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19-APR-2001
                                                                                             Center project name: bal80N18
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Center code: SC
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                                                                                                                                                                                                                 Center for Genome Research,
Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                     Submitted (07-APR-2001) to the EMBL/GenBank/DDBJ databases Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-ma
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                                                                                                                                                                                                                                               Draft Sequence Produced by
                                                                                                                                                                                                                                                                          humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.u)
                                                                                                                                                                                                                                                                                                                               Donnelly S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CATGTTAATTTCCCTTAGAAGTTCCAAGCCCTGTTTCCTGCGTAAAGGTGGTATGTCCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             standard; DNA; HTG; 183584 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel. 64, Created)
(Rel. 67, Last updated, Version
                                                                                                                                                                              Genome Center
                                                                                                                                                                                                                                                Whitehead Institute/MIT
                                                                                                                                                                                                                                   320 Charles Street,
    ham; 21% of reads
78% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23)
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Best Local Similarity
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Sequence 183584 BP; 45791 A; 43162 C; 44819 G; 49812 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    can tentatively be deduced from paired sequencing reads which have been identified to span the gap between two contigs. These are labelled as part of the same 'fragment_chain', and the order and relative orientation of the pieces within a fragment_chain is reflected in this file. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NOTE: This is a 'working draft' sequence. It currently consists of 1 contigs. The true order of the pieces is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   feature table.
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                                                                                                   TGCAATGTCTAAATCGCCTTAAAAGAGCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTT 2254
                                                                                                                                                   AGTCTTAATTAGGTACCTTATTAACAGGAAATGCTAAGGTACCTTCTCTGTGGAACAATC 2194
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/clone="RP11-180N18"
/clone_1ib="RPCI-11.1"
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Qy 2 Db	N	ОУ 2 Db	Qy 2	Qy 2 Db	Qy 2 Db	Query Best : Match	FEATURES SOURCE BASE COUNT ORIGIN	AUTHORS TITLE JOURNAL	SOURCE ORGANISM	LOCUS DEFINITION ACCESSION VERSION VERSION	RESULT :	Qy 2 Db 49	Qy 2 Db 49	Qy 2 Db 49	Qy 2 Db 49	Db 49
474 TICGAGITTTIAACTAGACTACACICTATI 2503 	4 0	354 GCGTAAAGGTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGGCTTGTTAAGATCA	294 GTAGGTTAGATGTGGGTGGTGCATGTTAAT [†] TTCCCTTAGAAGTTTCCAAGCCCTGTTTCCT 	234 CTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAGAAGCAGGGATGGTACCTACC	1174 TACCTTCTCTGTGGAACAATCTGCAATGTCTAAATCGCCTTAAAAGAGCCCATTTCTTAG	Match: 12.9%; Score 330; DE Local Similarity 100.0%; Pred. No. 1.7 es 330; Conservative 0; Mismatches	Location/Qualif Location/Qualif 1.376 /organism="Homo /db_xref="taxon /note="EMBL/Gen 125 a 78 c 8	Alvares,C Gene expr Patent: W	human SM Homo sapiens Eukaryota; Metazoa; Chordata; Crania Mammalia; Eutheria; Primates; Catarr	AX408384 376 bp Sequence 1031 from Patent WO0229103 AX408384 AX408384.1 GI:21441089	14	495 CACTCTATT 2503 942 CACTCTATT 49950	435 GTATAGCCCTTCCTCCACTCCCACCAGACTTGCTCATTTTTCGAGTTTTTAACTAGACT	375 TTCAGAGATGTGTATAATGAGCATGGCTTGTTAAGATCAGGAGGCCCACTTGGATTTAT 	315 CATGTTAATTTCCCTTAGAAGTTCCAAGCCCTGTTTCCTGCGTAAAGGTGGTATGTCCAG 	702 CACTTCTTCAGAGAAGCAGGGATGGTACCTACCCGGCAGGTAGGT
	4-4-	TGAGCATGGCTTGTTAAGATCA 2413	GAAGTTCCAAGCCCTGTTTCCT 2353 	AGGGATGGTACCTACCCGGCAG 2293	CTTAAAAGAGCCCATTTCTTAG 2233 	e-180; 0; Indels 0; Gaps 0	on NO. AA432168"	S. and Vockley, J.G. ncer 2;	ita; Vertebrata; Euteleostomi; hini; Hominidae; Homo.	DNA linear PAT 14-JUN-200			TTTCGAGTTTTTAACTAGACTA 2494 TTTCGAGTTTTTAACTAGACTA 49941	AGGAGGCCCACTTGGATTTATA 2434	TGCGTAAAGGTGGTATGTCCAG 2374 	GGTAGGTTAGATGTGGGTGGTG 49761

RESULT 15

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Search completed: April 20, 2003, 21:15:35 Job time : 6890 secs
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LOCUS
DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE
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                                                                                                2447 CTCCACTCCCACCAGACTTGCTCATTTTTCGAGTTTTTTAACTAGACTACACTCTATT 2503
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Sequence 40 from Patent WO0206317.
AX366273
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mitcham, J.L., King, G.E., Algate, P.A., Fling, S.P., Retter, M.W., Fanger, G.R., Reed, S.G., Vedvick, T.S., Carter, D., Hill, P. and Albone, E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/db_xref="taxon:9606"
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Human SAHH DNA #1.
Human SAHH DNA #2.
Human SAHH DNA #2.
Human prostate exp
Human colon cancer
Gene #1031 used to
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           Hart DNJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                       04-OCT-1996;
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                                                              (HART/) HART D'N J.
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/product= "DD4b5.3 enzyme"
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Best Local Similarity 100.0%; P
Matches 2563; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This is the nucleotide sequence of the DD4b9.3 enzyme which has S-adenosyl-L-homocysteine hydrolase (AHCY)-type activity. Its products can be used to identify substances which have a stimulatory or inhibitory effect on the enzyme activity. Such substances can be used to mediate dendritic cell (DC) function and for immunomodulation. They can be used in the treatment of e.g. autoimmune diseases, transplantations or cancers. The products can also be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 7; Fig 1; 33pp; English.
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P-PSDB; AAW56097.
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Pred. No. 0;
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CCCAGACAGGGGTGTGATTGAGACCATTGTGGCCCTGGGGGCTCAGTGCCGCTGCTGTTGTGCCCCAGAGGGCTTAAGCCTTGTGGCGCTTGTTGTGCAGGGGGTTGTTGTGCCAGGGGGTTGTTGTGCAGGGGGGGG		7	7	ெ	6	0 0	עכ	Ċ.	ū	ū	ίσ	44	4	w	w	32	w	2	N	N	N	$\dot{\mathbf{L}}$	-	0	0	0	0						4	œ	œ	Ñ	721
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                                                                       Human; prostate pharmacogenomic
         20-FEB-2001; 2001WO-US05171
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                                                        Homo sapiens
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                                                                                                                                                  ABV23195 standard;
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Score 2178; D. Pred. No. 0; O; Mismatches

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The invention relates to an isolated nucleic acid molecule (I) com a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: specification or its complement is afflicted with prostate cancer; (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                             cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(n a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
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                                                                   also useful as a pharmacodyanamic or pharmacogenomic marker.
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1440 1510	CGGGAGCACTT CGGGAGCACTT	1381 1451	
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1320 1390	TTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGGATGG	1261 1331	
1260 1330	TGTGTGGCTATGGTGAGGTAGGCAAGGCTGCTGTGCTGCTCTCAAAGCTCTTGGAGCAA	1201 1271	
1200 1270	CCATTTTGGÀTGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGG	1141 1211	
1140 1210	TGAACGTCAATĠATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAAT	1081	
1080 1150	TGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCA	1021	
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960 1030	TGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACT	901 971	
900 970	CAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTG		
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Human prostate expression marker cDNA 29023.

16-SEP-2002

(first entry)

ABV29032

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Query Match
Best Local Similarity 99.8
Conservative
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(d) assessing the eff
in a patient;
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18-JUL-2000;
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This sequence encodes a human S-adenosyl-5-homocysteine hydrolase (SAHH).

CC The SAHH protein can be used to generate specific antibodies and in drug CC screening to identify specific binding agents. Antagonists of the protein are used to treat or prevent a wide range of viral, bacterial, CC fungal, parasitic, protozoal or helminthic infections, many cancers (leukaemia, lymphoma or solid tumours), and many autoimmune diseases CC (e.g. acquired immune deficiency syndrome, allergy, asthma, diabetes CC mellitus, multiple solerosis etc). All these conditions may be treated by CC expressing antisense sequences, triplex-forming agents or ribozymes and directed against the nucleic acid. The nucleic acid and its fragments can be used as probes or primers for detecting and quantifying gene CC expression, for diagnosis or monitoring of disease, to identify genetic contactions, mutations or polymorphisms, in gene mapping and as antisense conditions, mutations or polymorphisms, in gene mapping and as antisense conditions are used directly as antagonists, indirectly to diseases in standard immunoassays, in competitive drug screens and to isolate the protein from natural sources.

Sequence 3616 BP; 1017 A; 782 C; 826 <u>.</u> 991 Η, 0 other;

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vulnerary; gastrointestinal; nephrotropic; antiinfective; yanecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.

Homo sapiens

WO200055174-A1

21-SEP-2000

08-MAR-2000; 2000WO-US05988

12-MAR-1999; 99US-0124270

(HUMA-) HUMAN (ROSE/) ROSEN GENOME SCI C A.

Rosen CA, Ruben MS

WPI; 2000-587513/55 P-PSDB; AAB56801.

disorders Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis such as prostate cancer

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Claim 1; Page 917-918; 2338pp; English

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to The prostate cancer antigens can have neuroprotective, cytostati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAB57303 represent sequences used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                or research purposes. The prostate cancer antigens may be used disorders such as neural, immune, muscular, reproductive,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Invention
                               653
                                                                                                   593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                176
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     reins, called prostate cancer antigens, given in AAB56363 to AAB57302 prostate cancer antigens can have neuroprotective, cytostatic,
                               CAGGÑAACGTGCTCAGGGGGA 673
                                                                                                                                                                                                                                                                                                                                       GAAGCCGACGCAGCTCGACGCAGGGGCCGGCAGGAGGGTGGGCGATCGCGTGTCGGAGGG
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                                                                                                                                                                                                  CCGTCGCTGTCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCA
CAGGAAACGTGCTCAGGGGGA
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                                                                                                                                                      GAAGCAGCAAACCAACTCCAAGGGCAGCAGCAGCATTTCTGTGTGAAGAACATCAAGCAGGC
                                                                                                                                                                                                                                                                                                                                                                                                           GGAGGAGCTGAAGCAGGCCAAGGAGTCGAGGACGCCGAGAAGTACTCCTTCATGGCCAC
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                                                                AGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACT
                                                                                                 AGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACT
                                                                                                                                   GAAGCAGCAAACCAACTCCAAGGGCAGCAGCAATTTCTGTGAAGAACATCAAGCAGGC
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99.8%;
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676
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Pred. No. 5.
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5.6e-208;
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AAV73925;

AAV73925 standard;

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Best Local (
                                                                                                                                                                                                                                                                                      Best Local Similarity 99.0 Matches 773; Conservative
                                                                                                                                                                                                                                                                                                                                                                             expressing antisense sequences, triplex-forming agents or ribozymes directed against the nucleic acid. The nucleic acid and its fragments can be used as probes or primers for detecting and quantifying gene expression, for diagnosis or monitoring of disease, to identify genetic variations, mutations or polymorphisms, in gene mapping and as antisense therapeutics. Antibodies are used directly as antagonists, indirectly to deliver active agents to SAHH-expressing cells, to diagnose and monitor diseases in standard immunoassays, in competitive drug screens and to isolate the protein from natural sources.
                                                                                                                            1848
                                                                                                                                                                                         1788
                                                                                                                                                                                                                        This sequence encodes a human S-adenosy1-5-homocysteine hydrolase (SAH protein can be used to generate specific antibodies and in dr screening to identify specific binding agents. Antagonists of the protein are used to treat or prevent a wide range of viral, bacterial, fungal, parasitic, protozoal or helminthic infections, many cancers,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acid encoding human S-adenosyl-5-homocysteine hydrolase for production of recombinant enzyme, useful for diagnosis, treatment and prevention of cancers, infections and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Corley NC, Hillman JIP Lal P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  S-adenosyl-5-homocysteine hydrolase; SAHH; human; treatment; infection; cancer; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (leukaemia, lymphoma or solid tumours), and many autoimmune diseases (e.g. acquired immune deficiency syndrome, allergy, asthma, diabetes mellitus, multiple sclerosis etc). All these conditions may be treated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 5; Column 39-42; 40pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diseases
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                                                                                                                                                         TGGACCATACTACCAAGGACCAGTCCACCTGAACCACACTCTAAAGAAATATTTTTTA
TTGTTTTTCATCTCATTATCCAAGTTCTGCAGACCACACAGGAACTTGCTTCATGGCTC
                                                            AGATAACTTTTATTTTCTTCTTACTCCTTTCCTCTTGATTTTTTTCCTATAATTTCATTC
                                                                                                                                                                                                                                                                                                                                                  2226
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                                                                                                                                                                                                                                                                                                                                                 649 A; 455 C; 435 G; 675 T; 12 other;
                                                                                                                                                                                                                                                                                                   21.6%;
99.6%;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                    DB 20;
1.5e-201;
hes 2;
                                                                                                                                                                                                                                                                                                                  Length 2226;
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detection; diag
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RESULT 7
ABV44141/c
ID ABV44141 £
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AC ABV44141;
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DT 16-SEP-200
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                                                                                                      09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, used for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                              Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                            Human prostate
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                                                                                                                                                                                                                     WO200160860-A2
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25-MAY-2000;
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                                                                                  MILLENNIUM
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                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                     ; 2000US-183319P.
; 2000US-189862P.
2000US-207454P.
; 2000US-211314P.
; 2000US-2119007P.
; 2000US-255281P.
                                                                                                                                                                                                                                                                                                                  (first
                                                              Endege
                                                                                                                                                                                                                                                                                             expression marker cDNA 44132
                                                                                                                                                                                                                                                               cancer;
marker;
                                                                                 PREDICTIVE MEDICINE
                                                                                                                                                                                                                                                                                                                                                           CDNA;
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                                                                                                                                                                                                                                                                                                                 entry)
                                                                                                                                                                                                                                                              cytostatic;
gene; ss.
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      tate of
useful
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RESULT 8
AAZ80766/c
ID AAZ80766 s
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AC AAZ80766;
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DT 07-APR-200
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DE Human colo
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KW Human; gen
KW colorectal
KW cytostatic
KW hyperplasi
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Best Local Similarity
Matches 422; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (d) assessing the efficacy or a control of a spatient; (e) selecting a composition for inhibiting prostate cancer in a patient; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                     1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement, (I) is useful for:
(a) assessing whether a patient is affilted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                        Human; gene expression product; diagnosis; tumour; colon colorectal adenocarcinoma; cell line SW480; cell prolife; cytostatic; sarcoma; breast cancer; neoplasia; dysplasia;
                                                                                                                                                                                                                                                                                                                                      1006
                                                                                               07-APR-2000
                                                                                                                                                                                                                                                                                     1066
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            hyperplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
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                                                                       cell
                                                                                                                                                cDNA;
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Pred. No. 1.8e-151;
                                                                       SW480 CDNA
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Best Local Similarity
Matches 370; Conserv
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Carroll E,
Schlegel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      the human colorectal adenocarcinoma (colon cancer) cell line SW480. The CDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The CDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia,
                                                                                  1056
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 469; 469pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     particularly cancers, especially colon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids, used to develop products for the diagnosis treatment of disorders involving unwanted cell proliferation,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 636 BP; 156 A; 166 C; 137 G; 147 T; 30 other;
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                                                                                                                                                                                                                                             TTCTGGTGGTGTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTG
                                                                                                                                                                                                                                                                                                      GCAGCACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGAC 875
                                                                                                                                                                                                                                                                                                                                                               CTGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCT 815
GATAACTTGT 1
                         GATAACTTGT 1125
                                                      GCTGGGAAGCTCTGTGTTCCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTT 1115
                                                                                                               ATCCGAGGCATTGTGGAAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAA 1055
                                                                                                                                                                      GATGATGGGGGAGACTTAACCCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAG
                                                                                                                                                                                                                               TTCTGGTGGTGTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTG
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                                                                                                                                                                                                                                                                                                                                                CTGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCT 311
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Catino TJ,
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100.0%; Pr
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, Derti A, Ford DM, Lewis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English.
                                                                                                                                                                                                                                                                                                                                                                                                                    Score 370;
Pred. No.
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ME, Monahan JE;
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                                                                                                                                                                                                                                                                                                                                                                                          expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful dagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-OCT-2000; 2000US-237054P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-APR-2002
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                                                                                                                                                                                        2234
                                                                                                                                                                                                                                      2174 TACCTTCTCTGTGGAACAATCTGCAATGTCTAAATCGCCTTAAAAGAGAGCCCATTTCTTAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from hepatocellular carcinoma in a patient, involving detecting the level of
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                                                           2354
                                                                                                                                                                                                                                                                                                                                                  Sequence 376 BP; 125 A; 78 C; 81 G; 92 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1031; 298pp; English
                                                                                                                                                                                                                     376
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                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                              ftp.wipo.int/pub/published_pct_sequences
                                                                                       GGAGGCCCACTTGGATTTATAGTATAGCCCCTTCCTCCACTCCCACCAGACTTGCTCATTT
                               GCGTAAAGGTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGGCTTGTTAAGATCA
                                              GCGTAAAGGTGGTATGTCCAGGTTCAGAGATGTGTATAATGAGCATGGCTTGTTAAGATCA
                                                                                                                                                        TACCTTCTCTGTGGAACAATCTGCAATGTCTAAAATCGCCTTAAAAGAGCCCCATTTCTTAG
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Pred. No. 2.4e-116;
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AAAA3426 to AAA45925 represent specifically claimed secreted expressed sequence tags (sESTs), isolated from human, mouse, chicken and rat tissue sources. The sESTs can have a range of activities depending on the tissues they were isolated from. The activities include:

CC chemotactic; proliferative; immunomodulatory; haematopoietic;

CC chemotactic; analgesic; haemostatic; thrombolytic; antidiabetic;

CC cytostatic; antibacterial; antifungal; antiviral; antidiabetic;

CC antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective;

CC antiasthmatic; antiparkinsonian; antipsoriatic; cerebroprotective;

CC antiasthmatic; and antidepressant. The sESTs can be used for gene therapy and in vaccines. The sESTs are useful as probes for the CC identification and isolation of full-length cDNAs and genomic DNA CC molecules which correspond to the sESTs. Proteins encoded by the SESTs are useful in assays for determining blological activity and raising care useful in assays for determining blological activity and raising can useful in assays for determining blological activity and raising can useful sclerosis, insulin dependent diabetes), allergic conditions (multiple sclerosis, insulin dependent diabetes), allergic conditions ulcers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disorders such as autoimmune, infectious, and central nervous system disorders.
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Treacy M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0104436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99WO-US24206
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Bowman MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INC
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RESULT 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
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                                                                                                                                                                                                                                                                            17-DEC-1998;
17-DEC-1998;
23-JUN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 349 BP; 98 A; 91 C; 87 G; 73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human ovarian carcinoma antigen polynucleotide SEQ ID NO:40.
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                                                                                                                                                                                                                                                       24-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                 17-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                 22-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200036107-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; ovarian carcinoma; ovarian cancer; therapy; diagnosis;
tumour antigen; identification; cytostatic; gene therapy; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAA69730;
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                                                                                                                                                                                                    (CORI-)
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                                                                                                                                                                                                                                                                               98US-0216003
99US-0338933
                                                                                                                                                                                                                                                                                                                                                                                    99WO-US30270
                                                                                                                                                                                                                                                       99US-0404879
                                                                                                                                                                                                                                                                                                                                 98US-0215681
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Pred. No.
                                                                                                                                                  PA,
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                                                                                                                                                    Frudakis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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Immunogenic portion of an ovarian carcinoma acid encoding it, useful for the diagnosis, cancer, preferably ovarian cancer.

protein and the nucleic prevention and treatment

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Claim 1;

F1g

1; 299pp; English.

describes an isolated polypeptide comprising

Query Match Best Local Similarity Matches 237; Conserv

Conservative

0,

Mismatches

9.2%;

Score 237; DB 21; Pred. No. 7.8e-81;

Length 292;

0

Gaps

276

216

97

Sequence 292 BP; 98 A; 68 C;

60 G; 66 T;

0 other;

exemplification of the present

invention.

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Mitcham :
Reed SG,
                                                                                        17-JUL-2000; 2000US-0617747.
10-AUG-2000; 2000US-0636801.
20-SEP-2000; 2000US-0667857.
04-APR-2001; 2001US-0827271.
18-JUN-2001; 2001US-08844441.
    Polypeptides comprising an immunogenic portion of a protein or its variants, useful for stimulating an patient and treating ovarian cancer -
                                    WPI; 2002-164781/21
                                                                                                                                       17-JUL-2001; 2001WO-US22635
                                                                          (CORI-)
                                                  JL, King GE, Vedvick TS,
                                                                         CORIXA CORP
                                                  Algate
Carter
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b. Albone
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bone E;
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sponse in
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24-JAN-2002. WO200206317-A2. Homo sapiens

immunostimulant;

cytostatic;

cancer; ovarian

carcinoma;

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immunogenic portion of an ovarian carcinoma protein (or its variants). Ovarian carcinoma proteins, and polynucleotides encoding them, have cytostatic activity and can be used in gene therapy and vaccines. Ovarian carcinoma polypeptides, nucleic acids, antibodies and vaccines are useful for the prevention, diagnosis and treatment of cancer, preferably ovarian cancer. AAA69691 to AAA70077 and AAB12552 to AAB12557 represent human ovarian carcinoma polynucleotides and proteins used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
RESULT 13
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AC ABL79
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Matches 237
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The present invention describes a composition (I) comprising: carriers and immunostimulants; and a polypeptide (II) of a ovarian tumour polypeptide encoded by a polypucleotide (III) having a DNA sequence (S1) from the 10912 nucleotide sequences as given in ABL77023 to ABL87934, (III) encoding (II) having a sequence (S2), a T cell
                                                                                                                                                                                                                            Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence represents DNA related to the invention.
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                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAY-2000; 2000US-207484P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-MAY-2001; 2001WO-US17756.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO200192581-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human ovarian cancer related cDNA clone SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-MAY-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABL79045 standard; cDNA; 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to polypeptides comprising an immunogenic portion of an ovarian carcinoma protein which acts as an immunostimulant and is cytostatic. The polypeptides, polynucleotic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CORI-) CORIXA CORP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 96
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cancer; ovarian tumour; cytostatic; gene;
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                                                                                                                                                                    489pp;
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Pred. No. 7.8e-81;
                                                                                                                                                                    English.
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96

CTCCACTCCCACCAGACTTGCTCATTTTTCGAGTTTTTAACTAGACTACACTCTATT 40 CTCCACTCCACCAGACTTGCTCATTTTTCGAGTTTTTAACTAGACTACACTCTATT

ILT 12 73634/c ABN73624 standard; DNA;

292 BP

ABN72624

Ovarian 02-JUL-2002

carcinoma antigen polynucleotide #40.

(first entry

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RESULTA14: 13
AAV06354/c
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           amount of polynuclectide hybridising to (IV) and comparing the amount to a predetermined cutoff value and thereby detecting ovarian cancer in the patient, where the amount of polynuclectide hybridising to (IV) is detected preferably by polymerase chain reaction (PCR). (I) comprising (III) and/or (II) is useful for stimulating and/or expanding T cells specific for an ovarian tumour protein comprising contacting T cells with (III) or (II). (III) is useful in design and preparation of ribozyme molecules for inhibiting expression of the tumour polypeptides and proteins in tumour cells; and to isolate a full length gene from a suitable library e.g., a tumour CDNA library using well known
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      population of (II), or antigen presenting cells that express (I(I) has cytostatic activity. An oligonucleotide (IV) that hybrid (S1) can be used for detecting ovarian cancer in a patient's bit sample preferably serum or ovarian tissue. The method comprises
                                                                                                                                                       mat_peptide
                                                                                                                                                                                                                                                                                                                    AL-21; AL-2; AL-2-long; human; treatment; neurological disorder; tumour; rheumatoid arthritis; wound healing; paralysis; anglogenesis; leukaemia; psoriasis; Alzheimer's disease; epilepsy; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                        30-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1382 TAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAA 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1322 GGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAA 1381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 553 BP; 159 A; 136 C; 128 G; 127 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                techniques.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contacting a biological sample from a patient with (IV),
                                                                                                                                                                        sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                      AL-2-long (AL-21) protein encoding DNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV06354;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAV06354 standard; DNA; 1877
                                                                                                                                                                                                                                                                                        Homo sapiens
               19-APR-1996;
                                           17-APR-1997;
                                                                           30-OCT-1997
                                                                                                            W09740153-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAA
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             9605-0635130
                                             97WO-US06345
                                                                                                                                                       /*tag= b
322..1608
                                                                                                                                                                                                                                       Location/Qualifiers 244..1611
                                                                                                                                                                                      /product= "AL-21"
244..321
                                                                                                                                                                                                                           *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the amount to cancer in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; Gaps
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biological
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AL-2 can be used as cognitive enhancer, to enhance learning particularly in dementias or trauma, since they can promote axonal outgrowth and synaptic plasticity, particularly of hippocampal neurons that express AL-2 binding Eph-family receptors and cortical neurons that express AL-2. AL-2 can also be used for wound healing, i.e. accelerating neovascularisation of, e.g. burns and ulcers. The encoding nucleic acids are useful in preparing antibodies that specifically bind to the AL-2 protein. The antibodies and the AL-2 antagonists are useful in diagnosing and treating various neuronal disorders. AL-2 antagonists can be used for modulating angiogenesis. They can also be used for the treatment of tumours, acute myeloid leukaemia (AML), chronic myeloid leukaemia (AML), chronic myeloid leukaemia (CML), myelodysplastic syndrome (MDS), diabetic retinopathy, neovascular glaucoma, psoriasis and rheumatoid arthritis.
                                                                                                                                                                                                                                                                                                                                                                   various conditions involving spinal muscular atrophy, or paralysis. AL-2 can be used to treat human neurodegenerative disorders, such as Alzheimer's disease, Parkinson's disease, epilepsy, demyelinating diseases such as multiple sclerosis, Huntingtons chorea, Down's Syndrome diseases such as multiple sclerosis, Huntingtons chorea, Down's Syndrome nerve deafness, Menier's disease, and other disorders of the cerebellum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malignancy, or toxic agents, to promote the survival or growth of neurons. They can be used to treat motoneuron disorders such as amyotrophic lateral sclerosis (Lou Gehrig's disease), Bell's palsy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     tyrosine kinase receptor ligand. AL-2 can be administered whom the nervous system has been damaged by trauma, surger ischaemia, infection, metabolic disease, nutritional defic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      products for, e.g. treating neurologic disorders, angiogenes, disorders, tumours or rheumatoid arthritis or for wound heal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This DNA encodes a AL-2-long (AL-21) protein. AL-2 is a novel Eph-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Fig 1A-C; 86pp; English
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    used to

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and AL-2

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RESULT 15
ABN93848
ID ABN93
XX
AC ABN93
XX
DT 13-AI
XX
DT 13-AI
XX
XX
Gene
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Best Local
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                                                                                                                        ABN93848 standard; DNA;
                                                                                                                                                                                                                                                                                                                                                                                 1446 CCCCATCTGTGCTCTGCAGGCCTGCATGGATGGGTTCAGGGTGGTAAAGCTAAATGAAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1877 BP; 334 A; 525 C; 615 G; 401 T; 2 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                     CATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATGTAGTGACACGGGA
                                                                                                                                                                                                                                                                         GCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACACAGA
                                                                                                                                                                                                                             AATCGATGTG 1472
                                                                                                                                                                                                                                                            GCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACAC
                                                                                                                                                                                                                                                                                                                     CATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATGTAGTGACACGGGA
                                                                                                                                                                                                                                                                                                                                                                                                                                               190;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                            7.4%; Score 190; DE
100.0%; Pred. No. 5.1
1ve 0; Mismatches
                                                                                                                        384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 1877;
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B Š 밁 Ş 밁 Ş 밁

Gene; liver cancer; ds; hepatocellular carcinoma; hepatotropic;

Gene #346 used to diagnose liver cancer.

13-AUG-2002 ABN93848;

(first entry)

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metastatic liver tumour; cytostatic; expression profile; disease state; disease progression; drug toxicity; drug efficacy; drug metabolism.
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02-OCT-2001; 2001WO-US30589.

02-OCT-2000; 2000US-237054P.

(GENE-) GENE LOGIC INC.

Horne D, Alvares C, Peres-Da-Silva S, Vockley JG;

Diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumor in a patient, involves detecting the level of expression of two or more genes in a iver tissue sample

Claim 1; SEQ ID NO 346; 298pp; English

expression of two or more genes represented in ABN93503-ABN97455 in a tissue sample. The method of the invention has hepatotropic, and cytostatic activity. The method is useful for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma and metastatic liver carcinoma in a patient. The method is useful for identifying expression profiles which serve as useful diagnostic markers as well as markers that can be used to monitor disease states, disease progression, drug toxicity, drug efficacy and drug metabolism.

Note: The sequence data for this patent did not form part of the printed as pecification, but was obtained in electronic format directly from WIPO The invention relates to a novel method for diagnosing and detecting the progression of liver cancer, hepatocellular carcinoma or metastatic liver tumour in a patient, and differentiating metastatic liver cancer from nepatocellular carcinoma in a patient, involving detecting the level of expression of two or more genes represented in ANN93503-ANN97455 in a rissue sample. The method of the invention has hepatotropic, and ftp.wipo.int/pub/published_pct_sequences

Sequence 384 BP; 95 A; 77 C; 113 G; 99 T; 0 other;

밁 Query Match Best Local Similarity Matches 168; Conserv 1065 CTCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTG 1124 73 CTCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTG 132 Conservative 6.6%; but 100.0%; pr Score 168; DB 24; Length 384; pred. No. 1.6e-54; 0; Mismatches. 0; Indels 0; Gaps 0

밁 133 TACTGCTGCCGAGAATCCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGTTTGGT 192

1125 TACTGCTGCCGAGAATCCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGTTTGGT 1184

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문 Ş 1185 GGGAAACAAGTGGTGTGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGC 1232 193 GGGAAACAAGTGGTGGTGTGGCTATGGTGAGGTAGGCAAGGGCTGC 240

Search completed: April 20, 2003, 19:20:50 Job time : 561 secs

Result a a 000 ESSION ESSION ö ERENCE UTHORS ITLE WORDS TRCE PRGANISM ULT 1 29176 US score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. 1288. 1001. 1001. 403.6 400.4 377.8 376.6 2161 404 806 806 703 703 703 703 703 488 488 488 421 421 421 Sequence 1 AX029176 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2563)
Hart, D.N.
Hart, D.N.
Enzyme having s-adenosyl-1-homocysteine hydrolase (ahcy) type
activity human AX029176.1 GI:10190060 AX029176 100.0 100.0 98.8 Match 80423 175335 223098 338234 2067 190612 5050 40320 172372 183584 1792 2563 bp from Patent WO9814562. 1603 DB MUSSAHH BC015304 AC129093 DMBX200 AX458351 AC091636 AE003715 DMU31961 AY102668 DMAHCYGEN AX408384 AF080546 LEISADSH RATAHHA HUMAHCY2 AK097610 SUMMARIES ALIGNMENTS DNA linear AR068569 Sequence
AX069339 Sequence
AX772411 Human DNA
A1360171 Human DNA
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Database

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Post-processing: Minimum Match 0% Maximum Match 10

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Total number of hits satisfying chosen parameters:

4109280

2054640 seqs, 14551402878 residues

Title: Perfect score:

US-09-782-051-1 2563

ggcgcgggcaggtcggagct....

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Scoring table: Sequence:

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GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.

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CCAAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCCTCACTGACAGCTACA 480 [/ Match Local Similarity 100.0%; Score 2563; DB 6; Length 2563; Local Similarity 100.0%; Pred. No. 0; les 2563; Conservative 0; Mismatches 0; Indels 0; Gaps 0; les 2563; Conservative 0; Mismatches 0; Indels 0; Gaps 0; les 2563; Conservative 0; Mismatches 0; Indels 0; Gaps 0; les 2563; Conservative 0; Mismatches 0; Indels 0; Gaps 0; les 2563; Conservative 0; Mismatches 0; Indels 0; Gaps 0; les 2563; Conservative 0; Mismatches 0; Indels 0; Gaps 0; les 2563; Conservative 0; Mismatches 0; Indels 0; Gaps 0; les 2563; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0; les 2563; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Gaps 0; les 2563; Conservative 0; Mismatches 0; Indels 0; Indels 0; Gaps 0; Gaps 0; Gaps 0; les 2563; Conservative 0; Mismatches 0; Indels 0; In	/note="Open reading frame extends without a stop codon for the full 5' nucleotide sequence. The initiation codon has yet to be identified." /codon_start=1 /protein_id="CAC09285.1" /db_xref="G1:10190061" /translatton="RCOVGRARSCCEWPSCGHRRCPAALGCRTDKAWATAPQKPTQLDA GAGRRVGDRVSEGAARAGGRAPEGERGGGGSAAGRAGGGMSMPDAPLPGVGEELKQ AKELEDAEKYSFMATVTKAPKKOIQFADDMOETKNEFPTKTGRRSLSRSJSOSSTDSYS SAASYTDSSDEVSPREKQOTNSKGSSNFCVKNIKQAEFGRREIEIAPQDMSALISLR KRAGCEKPLAGAKIVGCTHITAQTAVLIETLCALGAQCRWSACNIYSTQNEVAAALAE AGVAVPAWKGESEDDEWGCIDRCVNMDGWQANMILDDGGDLTHWYYKKYPNVFKKIRG IVESVTGVHALGALSTLOCKNADSWOKFPNLYCCESILDGLKRTTDVM FGGKQVVVCCYGGEVGKCCAALKAGAIVYITEIDPTCALGACMDGFRVKKLHSVIRQ VDVVITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLRTPELTWERVVRAUVD VTKCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLRTPELTWERVRSQVD HVHPDGKRVVLLAEGRLLNLSCSTVPTFVLGITATTQAALILELTNAPEGRYKQDVY LLPKKMDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGPFKPNYXK" 646 a 604 c 677 g 636 t	Patent: WO 9814562-A 1 09-APR-1998; HART DEREK NIGEL JOHN (NZ) LOCATION/Qualifiers 1. 2563 /organism="Homo sapiens" /db_xref="taxon:9606" <3. 1847
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Mammalla; Eutherla; Prin
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Primates;
         Angel, N.Z.,
                       Craniata; Vertebrata; i Catarrhini; Hominidae;
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          Clark, G.J.
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Submitted (23-OCT-2000) Dendr
Research Institute, Level 3,
Queensland 4101, Australia
Location/Qualifiers
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Dekker,J.W., Budhia,S.,
Hart,D.N.J. and Kato,M.
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Submitted (10-JUL-2001) National Institutes of Health, Mammalian Submitted (10-JUL-2001) National Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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This clone was selected for full length sequencing because
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Villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S., I
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck,
Muzny,D.M., Gibbs,R.A.
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/db_xref="LocusID:10768"
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/protein_id="AAH10681.1"
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                                                                                                                                                                 Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortlum/LLNL at: http://image.llnl.gov Series: IRAK Plate: 20 Row: a Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens, S-adenosylhomocysteinewhydrolase-like 1, clone MGC:21453 IMAGE:3450568, mRNA, complete cds.
                                                                                                                                                                                                                                                                                                                                        cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mod@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (05-NOV-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC Project URL: http://mgc.nc1.n1h.gov
Contact: MGC help desk
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1 (bases 1 to 2552)
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Tissue Procurement: ATCC
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/clone="MGC:21453 IMAGE:3450568"
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/db_xref="taxon:9606"
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Best Local Similarity 99.1
Matches 2549; Conservative
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644
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VDHYUMPDGKRVVLLAEGRLLNLSCSTVFTFVLSITATTQALALIELYNAPEGRYKQD
VYLLPKKNDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGPFKPNYYRY*
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/note="Vector: pCl
338. .1840
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                          NIH-MGC Project URL: http://mgc.nc1.nih.Contact: MGC help desk
                                                                 Direct Submission
Submitted (10-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                  Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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| W. (bases 1 to 2526)
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cgapbs-r@mail.nih.gov
Procurement: ATCC
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.series: IRAL Plate: 22 Row: h Column: 21
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency Okanalysis, Similarity but not identity to protein.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
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TSSAASYTDSSDDEVSPREKQQTNSKGSSNFCVKNIKQAEEGREIEIAEQDMSALIS
LRKRAQGEKPLAQAKIVGCTHITAQTAVLIETLCALGAQCRWSACHIYSTOMEVAAAL
AEAGVAVFAWKGESEDDFWWCIDRCVNMDGWQANMILDDGGDLTHWVYKKYPNVFKKI
RGIVEESVTGVHRLYQLSKAGKLCVPANNVNDSVTKQKFDNLYCCRESILDGLKRTTD
VMFGGKQVVVCGYGEWFKGCCAALKALGAIVITIEIDPICALQACMDFFRYVKLNEVI
RQVDVVITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLRTPELTWERVRSQ
VDHVIMPDGKRVVLLAEGRLLNLSCSTVFTFVLSITATTQALALIELIXNAPEGRYKQD
VTLLPKKMDEVYNSLHLPSFDAHLTELTDDQAKYLGLNKNGPFKPNYYRY

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/db_xref="LocusID:10768"
/db_xref="taxon:9606"
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/protein_id="AAH07576.1"
/db_xref="GI:14043177"
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/clone_lib="NIH_MGC_21"
/lab_host="DH10B-R"
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Complementation of chromosomal instability in the xeroderma pigmentosum variant by a gene on human chromosome 1 with homology to S-adenosyl homocysteine hydrolase
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Increased ultraviolet sensitivity and chromosomal instability related to P53 function in the xeroderma pigmentosum variant Cancer Res. 59 (5), 1102-1108 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (19-DEC-1996) Dermatology, 0750, San Francisco, CA 94143, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
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Volpe, J.P.G., Busch, D.B., Coleman, D.M., Ziffer, 1
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                                                                                                                             /product="S-adenosyl homocysteine hydrolase homolog"
/protein_id="AAC01960.1"
/db_xref="G1:2852125"
/translation="MARVYKAPKKOIOFADDMOEFTKFFTKTGRRSLSRSISQSSTDS
/translation="MARVYKAPKKOIOFADDMOEFTKFFTKTGRRSLSRSISQSSTDS
YSSAASYIDSSDDEVSFREKQQINSKGSSNFCVKNIKQAEFGRREIEIAEQDMSALIS
LRKRAQGEKFLAGAKIYGCTHITAQTAVILETLCALGACRWSACNIYSTQNEVAAAL
AEAGVAVFAMKGESEDDFWMCIDRCVNNDGMQANMILDDGGDLTHWYYKKYPNVFKKI
RGIVESSYTGYHRLYQLSKAGKLCVFANHVNDSYTKQKFDNLYCCRESILDCKRFTD
VMFGGKQVVVGGYGEVGKGCCAALKALGAIVYITEIDFICALQACMDGFRVVKLNEVI
RQVDVVITCTGKKNVVEREHLDRKKNSCIYCINKGHSNTEIDVTSLRTPELTWERVRSQ
VDHYLMPDGKRVVLLAEGRILNLSCSTYPTFVLSITATTQALALIELIYNAPEGRYKQD
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                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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CCAGACTTGCTCATTTTTCGAGTTTTTAACTAGACTACACTGTA-TTGAGTTTAATTTTG
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Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further
information about the clone and the sequencing project is av
at http://www.mips.biochem.mpg.de/proj/cDNA/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequence consortium of the German Genome Project.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Martinsried, GERMANY
Clone from S. Wiemann,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2510)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-MAY-1999) MIPS,
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                                                                        Conservative
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                                                                                                                                                                                                                                     /translation-"GLLTVELDSSCVCYILLLLRHRGGSRRGKICAEISQPALPLPQE
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CCAALKALGAIVYITEIDPICALQACMDGFRVVKLNEVIRQVDVVITQTGNKNVVTRE
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splice variant"
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/clone_lib="564 (synonym: hfbr2). Vector
X1-2blue; sites NotI + SalI"
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/db_xref="GI:4884204"
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/db_xref="taxon:9606"
/map="1, 15.55 cR from D:
/clone="DKFZp564A1523"
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	1573	4 TTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCTCCTGGCAGAGGG	y 1514
	1513 1462	4 CAACACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCGAGTACG	y 1454 b 1403
	1453 1402	GACACGGGAGCACTTGGATCGCATC	
	1393 1342	AAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCAC 	νω
	1333 1282	4 CGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGGATGG) 1274 5 1223
	1273 1222	4 TGAGGTAGGCAAGGGCTGCTGTGCTGCTCTCAAAGCTCTTGGAGCAATTGTCTACATTAC 	y 1214 o 1163
	1213 1162	4 CCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGCTATGG 	y 1154 b 1103
	1153 1102	4 TTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTGGATGG 	y 1094 b 1043
	1093 1042	4 CAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACGTCAATGA 	у 1034 Б 983
	1033 982	4 GTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGAAGAGAGCGTGACTGGTGTTCA 	y 974 b 923
	973 922	4 GTGGCAGGCCAACATGATCCTGGATGATGGGGGGAGACTTAACCCACTGGGTTTATAAGAA 	y 914 b 863
	913 862	4 GAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTGTGAACATGGATGG	y 854 5 803
	853 802	4 CTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTTG	y 794 o 743
	793 742	4. GTTGATTGAGACACTCTGTGCCCTGGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTA 	y 734 b 683
,	733 682	4 GAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACACACATCACAGCCCAGACAGCCGGT	y 674 b 623
	673 622	4 TGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGA 	y 614 b 563
	613 562	4 GGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGCAGGCAG	y 554
	553 502	4 CTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGCAAACCAACTCCAA	y 494 b 443
	493 442	4 AAGATCTTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACAGTTCAGCTGCATC	y 434

CTGTTGTCC	2481	Дb
TCTGTTGTCCAAAAAAAAAAAAAAAAAAAAA 2563	2534	Qy
TTCGAGTTTTTAACTAGACTACACTCTA-TTGAGTTTAATTTTGTCCTCTAGGATTTATT	2422	Дb
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GAAGGCCCACTTGGATTTATAGTATAGCCCCTTCCTCCACTCCCACCAGACTTGCTCATTT	2362	뫄
GAGGCCCACTTGGATTTATAGTATAGCCCTTCCTCCACTCCACCAGACTTGCTCATT	2414	ρ
GCGTAAAGGTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGGCTTGTTAAGATCA	2302	₽
CGTAAAGGTGGTATGTCCAGTTCAGAGATGTGTATAATGAGCATGGCTTGTTAAGATC	2354	Qy
TAGGTTAGATGTGGGTGCATGTTAATTTCCCTTAGAAGTTCCAAGCCCTGTTTCC	2242	Дb
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TCTGCAGACCACAGGAACTTGCTTCATGGCTCTTTAGATGAAATAGAAGTTCAGGGTT	1943	Db.
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CTTTCCTCTTGATTTTTTCCTATAATTTCATTCTTGTTTTTTCATCTCATTATCCAAGT	1883	밁
TTTCCTCTTGATTTTTTTCCTATAATTTCATTCTTGTTTTTTCATCTCATTATCC	1934	δõ
ACCTGAACCACACTCTAAAGAATATTTTTTNAGATAACTTTTATTTTCTTCTTACTC	1823	망
CCTGAACCACACTCTAAAGAAATATTTTTTAAGATAACTTTTATTTTCTTCTTAC	1874	Q .
TGGGCCATTCAAACCTAATTATTACAGATACTAATGGACCATACTACCAAGGACCAGTCC	7	В
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TGTACTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGCTTGCCATCTGCCATC	1643	D G
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CACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGCGATACAAGCAG	1583	рb
ACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGCGATACAAGCAGG	1634	Ωy
TCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCACAGCCAC	1523	В
CGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCATCACAGCCA	1574	Qy
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BC018218 BC018218 GI:17390492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
Sequencing Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (03 DEC-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clone distribution: MGC clone distribution information can be for through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.gov series: IRAK Plate: 23 Row: n Column: 6 This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
Yoon, V.S., Kowlé, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
Richards, S., Gibbs, R.A.
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Contact: MGC help desk
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                                                                                                                                                    /Traiblation="MATVTKAPKKQIQFADDMQEFIKFPIKTGRRSLSRSISQSSTDS
YSSAASYTDSSDDEVSPREKQQTNSKGSSNFCVKNIKQAEFGRREIELAEQDWSALIS
KRKRAQGEKPLAGAKIYGCTHITAQTAVLIETLCALGAQCRWSACNIYSTQNEWAALA
AEAGYAVFAWKGESEDFWGCIDRCVMMDGWQAMMILDDGGDLTHWYVKKYPNVFKKI
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VMFGGKQVVVCGYGEVGKGCCAALKALGAIYYITEIDFICALQACMDGFRYVKLNEVI
                                                                                                    RQVDVVTTCTGNKNVYTREHLDRMKNSCIVCNMGHSNTEIDVTSLRTPELTWERVRSQ
VDHVIWPDGKRVVLLAEGRLLNLSCSTVPTFVLSITATTQALALIELYNAPEGRYKQD
VYLLPKKMDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGPFKPNYYRY"
                                                                                                                                                                                                                                                                      /product="S-adenosylhomocysteine hydrolase-like
/protein_id="AAH18218.1"
/db_xref="GI:17390493"
                                                                                                                                                                                                                                                                                                                                                                                                                  enhancer
                                                                                                                                                                                                                                                                                                                                                              /note="Vector: pCMV-SPORT6"
                                                                                                                                                                                                                                                                                                                                                                                /lab_host-"DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                /tissue_type="Mammary tumor metastatized to lung.
MMTV-LTR/Wntl model. Expression driven by an MMTV-LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Mus musculus"
/db_xref="taxon:10090"
/map="CZECH II"
/clone="MGC:18748 IMAGE:4007102"
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(bases 1 to 1369)
2 (bases 1 to 1369)
Yu,W., Andersson,B., Worley,K.C., Muzny,D.
Yu,W., Andersson,B., Wentland,M.A., Lennon,G.
Ricafrente,J.Y., Wentland,M.A., Lennon,G.
Large-scale concatenation cDNA sequencing
Genome Re
97264341
9110174
                                                                        Eukaryota; Metazoa; Chordata; Craniata;
Mammalia; Eutheria; Primates; Catarrhin
1 (Bases 1 to 1369)
Andersson, B., Wentland, M.A., Ricafrente
A b double adaptor' method for improved
Anal. Biochem. 236 (1), 107-113 (1996)
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                                         Liu, W.,
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Query Match
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                            ATCTGCCATCATTTGATGCCCACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGG
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ATGCACCCGAGGGGCGATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAAT 1725 [GCAAACGAGTTGTCCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTC 369 CCACCTTTGTTCTGTCCATCACAGCCACACACACACGCTTTGGCACTGATAGAACTCTATA 1665	GTTGTATCGTATGCATATGGGCCACTCCAACACAGAAATCGATGTGACCAGCCTCCGCA 249 CTCCGGAAGCTGACGTGGGAGCAGATACGTTCTCAGGTGGACCATGTCATCTGGCCAGATG 1545 [/ Match 50.3%; Score 1288.8; DB 9; Length 1323; Local Similarity 99.7%; Pred. No. 6.4e-251; hes 1312; Conservative 0; Mismatches 2; Indels 2; Gaps 2; les 1312; Conservative 0; Mismatches 2; Indels 2; Gaps 2; les 1312; Conservative 0; Mismatches 2; Indels 2; Gaps 2; les 1312; Conservative 0; Mismatches 2; Indels 2; Gaps 2; les 1312; Conservative 0; Mismatches 2; Indels 2; Gaps 2; les 1312; Conservative 0; Mismatches 2; Indels 2; Gaps 2; les 1312; Conservative 0; Mismatches 2; Indels 2; Gaps	/protein_id="AAH03631.1" /protein_id="AAH03631.1" /db_xref="GI:1317703" /db_xref="GI:1317703" /translation="HeealgarvyITeIdpICALQACMDGFRVVKLNEVIRQVDVVI /translation="HeealgarvyITeIdpICALQACMDGFRVVKLNEVIRQVDVVI /CTGNKNVVTREHLDBAKKNSCITVCNMGHSNTEIDVTSLRTPELTYMERVRSQVDHVLWP CTGNKNVVTREHLDBAKKNSCITATTQALALIELTWAPEGRYKQDVYLLPKK GKRVVLLAEGRILINLSCSTVPTFVLSITATTQALALIELTWAPEGRYKQDVYLLPKK GKRVVLLAEGRILINLSCSTVPTFVLSTTATTQALALIELTWAPEGRYKQDVYLLPKK GKRVVLAEGRILINLSCSTVPTTATTQALAEGRILINLSCSTVPTTATTQALAEGRILINLSCTTATTATTATTATTATTATTATTATTATTATTATTATTA	/db_xref="taxon:9606" /clone="IMAGE:3010755" /tissue_type="Muscle, rhabdomyosarcoma" /clone_lib="NIH_MGC_17" /lab_host="DH10B-R" /note="Vector: pOTB7" <1. 611 /product="Similar to S-adenosylhomocysteine hydrolase-like	Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAL Plate: 3 Row: b Column: 6. Location/Qualifiers 11323 ce /organism="Homo sapiens"	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadanesystemsbiology.org contact: ATCC Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephanie Ford, Julia Greene, Mark Ketteman and Anuradha Madan

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Series: IRAL Plate: 23 Row:
Location/Qualifiers
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Tissue Procurement: DCTD/DTP
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Contact: MGC help desk
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VITCTGNKNYTTREHLDRAKKNSCIVCUMGHSNTEIDPASLTREPELTWERFYRSQVDHYI
WPDGREIVLLAEGRILNHISCSTYPTFVLSITATTQALALIELYNAPEGFKKQDYYLLP
KKMDEYYASLHLPTFDAHLTELTDEQAKYLGLNKNGPFKPNYYRY"
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SYTDSSDDETSPRDKQQKNSKGSDFCKNIKQAEFILEIABQEALMALKKRA
QGEKPLAGAKIVGCTHITAQTAVLMETLGALGAQCRWAACNIYSTLNEWAALAESGF
FVFAWKGESEDDFWCIDRCVNVEGWQPNMILDDGGDLTHWIYKKYPNMFKKIKGIVE
ESYTGVHRLYQLSKAGKLCVPAMNYNDSVTKQKFDNLYCCRESILDGLKŘTTDMMFGG
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/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
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/db_xref="GI:14249936"
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/db_xref="taxon:9606"
/clone="IMAGE:3536052"
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                                  AGAGCACTTGGACCGTATGAAGAATAGCTGCATCGTTTGTAACATGGGACATTCCAACAC
                                                                  GGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCCACTCCAACAC 1459
                                                                                                         GGTCATCCGACAAGTGGACATTGTTATTACCTGTACAGGTAACAAGAATGTGGTAACCAG
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Homo sapiens, K
mRNA, complete
                                                                                                                                  Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLNL at: http://image.linl.gseries: IRAK Plate: 22 Row: 1 Column: 22
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) cDNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Contact: MGC help desk
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/db_xref="taxon:9666"
/clone="MGC:21525 IMAGE:3907552"
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                                                                                                                  Location/Qualifiers
/tissue_type="Uterus, leiomyosarcoma"
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AGGGDPEAPAPAAERPPVFGPGSGPAAALSPAAGKVPASAMKRSDPHHOHQRHROG
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KQVVVCGYGEVGKGCCAALKAMGSIVYVTEIDPICALQACMDGFRLVKLNEVIRQVDIV
VITCTGNKNVTREHLDRMKNSGIVYCHENDIDFICALQACMDGFRLVKLNEVIRQVDIV
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WPDGKRIVLLAEGRILMLSGSTVPFFVLSITATTQALALIELYNAPEGRYKQDVYLLP
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/lab_host="DH10B"
/note="Vector: pCMV-SPO
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                                                                                                                                               AAGAGGCGGGGGCGGCTCAGCCGCTGGCCGGGCCGGGGGGAATGTCGATGCCTGA 268
                                                                                                                                                                             Submitted (02-DEC-1998) Osamu Ohara, Razusa Laboratory of DNA Technology; Yana 1532-3, Laboratory Japan (E-mail:cdnainfo@kazusa.or. Fax:+81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase,T., Ishikawa,K., Suyama,M., Kikuno,R., Hirosawa,M., Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro DNA Res. 5 (6), 355-364 (1998)
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Chare, O., Suyama, M., Kikuno, R., Nagase, T. and Ishikawa.
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/protein_id="BAA74851.1"
/db_xref="G1:4240145"
/db_xref="G1:4240145"
/translation="EPVVAAEAVMSYQYVSAAAAAKVPEVELKDLSPSEAESQLGLST
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KKIKGIVEESYTGVHRLYQLSKAKKLOVAAMGSIVYVTEIDPICALQACMGFRLVKLN
EVIRQVDIVITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVASLRTPELTWERV
RSQVDHYIRPDGKRIVLLAEGGELLNLSGSTVFYFTLSITATQALALIELINAPEGRY
RSQVDHYIRPDGKRIVLLAEGGELLNLSGSTVFYFTLSITATQALALIELINAPEGRY
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/clone_lib="pBluescriptII
/dev_stage="adult"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                 Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnai@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-546)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Watanabe, K., Kumagai, A., Itakura, S., Yamazaki, M., Tashiro, H., Ota, T., Suzuki, Y., Obayashi, M., Nishi, T., Shibahara, T., Tanaka, T., Nakamura, Y., Isogai, T. and Sugano, S.
NEDO human cDNA sequencing project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1987 bp mRNA linear Homo sapiens cDNA: FLJ21719 fis, clone COLF0094. AK025372
                                                                                                                                                                                                                                                  NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Blotechnology; cDNA llbrary construction, 5'- & 3'-end one pass sequencing: Departent of Viscology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                            construction, 5'- & 3'-end one pass seque virology and Human Genome Center, Institutionarity of Tokyo (partly supported by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 1987)
Sugano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi,T., Isogai,T.,
Shibahara,T., Tanaka,T. and Nakamura,Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens colon mucosa cDNA to mRNA, clone_lib:ColF
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/tissue_type="colon mucosa"
/clone_lib="coler"
/note="cloning vector pME18SFL3"
/430 c 501 g 499 t
                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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1. .1987
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  1276 GGTGAAATTAAATGAGGTCATCCGACAAGTGGACATTGTTATTACCTGTACAGGTAACAA
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1384	25 GGTAAAGCTAAATGAAGTCATCCGGGCAAGTCGÁTGTCGTAATAACTTGCACAGGAAATAA	Qy 13	
1275	CTGAAATTGACCCCATCTGTGCCCTGCAAGCCTGTATGGATGG	рь 12	
1324	ATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGGATGG	Qy 12	
1215	GGGCTCCATTGT	рь 11	
1264	GGCTATGGTGAGGTAGGCAAGGGCTGCTGTGCTGCTCTCAAAGCTCTTTGGAGCAATTGT	Qy 12	
1155	CTTGATGGACTTAANAGGACAACAGACATGATGTTTGGTGGAAAGCAAGTGGTAGTCTG	Db 10	
1204	ATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGT	Qy 11	
1095	36 TGTCAATGACTCAGTCACCCAAACAGAAATTTGACAACCTCTACTGTTGCCGTGAATCAAT	10	
1144	NATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCAT	10	
1035	6 TGGAGTTCACAGGCTGTACCAACTGTCCAAAGCTGGGAAGCTGTGTGTTCCAGCCATGAA	Db 97	
1084	GGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCCGGCCATGAA	Qy 10	
975	16 TATAAAAAGTATCCCAACATGTTTAAGAAANTCAAGGGCATAGTAGAGGAGAGTGTTAC	9 da	-
1024	ATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGGAAGAGAGCGTGAC	Оу 9	
915	56 TGTGGAGGCCTGCCAAACATGATCTTGGATGATGAGGGGATCTTACCCACTGGAT	р ъ 8	•
964	ATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACTGGGT	Оу 9	
855	TTGCCTGGAAGGGAGAGTCAGAAGATGACTTCTGGTGGTGTATCGATAGATGTGTGAA	Db 7	
904	GAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTGTGAA	Оу в	
795	36 CAACATCTATTCCACTCTCAATGAAGTGGCTGCTGCTGCTGCAGAAAGTGGATTTCCTGT	Db 7	
844	CATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTGCAGT	Qy 7	
735	TTATGGAAACTCTGGGTGCTCTGGGGGCCCAGTGCCGATGGGCTGCCTG	6	
784	CAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGGCTCAGTGCCGCTGGTCTGCTTG	Qy 7	
675	CTCA	Db 6	
724	agggggagaagcccttggctggtgctaaaatagtgggctgtacacacatcacagccca	Оу 6	
615	56 AAGAGAAATTGAAATTGCTGAACAAGAAATGCCTGCATTGATGGCTTTGAGGAAGAGAGC	U	
664	ATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGC	оу б	
555	TANGGGAAGCAGTGACTTCTGTGTTAAGAACATCAAACAGGCAGAGTTTGGACG	Db 4	
604	TCCAAGGGCAGCAATTTCTGTGTGAAGAACATCAAGCAGGCAG	Оу 5	
495	CATCGCCCAGGGACAAGCAGCAAAA	Db 4	
544	CTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGCAAAC	Оу 4	
435	76 AATTGGACGTCGCTCTTGTCTCGTTCCCATTTCTCAGTCATCTACTGACAGCTACAGCTC	Db 3	
484	TGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACAGTTC	Qy 4	
375	16 GCCTGAGTGGATCAGTTTGCTGACCAGAAGCAAGAATTCAACAAACGTCCCACCAA	Db 3	
424	CCCAAGAAGCAAATCCAGTTTGCTGATGACATGCAGGAGTTCACCAAATTCCCCCACCAA	Ωγ 3	
Bd	Match 38.3%; Score 982.2; DB 9; Length 1987; Local Similarity 78.2%; Pred. No. 9.6e-189; Res 1179; Conservative 0; Mismatches 328; Indels 0; Ga	Query Best Match	
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Hest Local Similarity 99.3%;
Matches 830; Conservation
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                 1848 TGGACCATACTACCAAGGACCAGTCCACCTGAACCACACTCTAAAGAAATATTTTTTA 1907
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                                            GCGAGTGAGATCTCAAGTTGACCATGTGATATGGCCTGATGGCAAGAGGATAGTACTGCT 1515
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                                                                                                                                                                                                                                                          Unclassified.
Unclassified.
1 (bases 1 to 2226)
1 (bases 1 to 2226)
1 (liman, J.L., Corley, N.C., Lal, P. and Shah, P. Hillman, J.L., Corley human S-adenosyl-5-homocysteine hydrolase Polynucleotides encoding human S-adenosyl-5-homocysteine hydrolase derived from bladder
Patent: US 5854023-A 2 29-DEC-1998;
Location/Qualifiers
2226
2226 bp
Sequence 2 from patent US 5854023.
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2507 778	TCCACTCCCACCAGACTTGCTCATTTTTCGAGTTTTTAACTAGACTACACTCTATTTGAG	2448 720	Qy Db
2447 719	ATRATGAGCATGGCTTGTTAAGATCAGGAGGCCCACTTGGATTTATAGTATAGCCCTTCC	2388	ДУ
2387 659	CTTAGAAGTTCCAAGCCCTGTTTCCTGCGTAAAGGTGGTATGTCCAGTTCAGAGATGTGT	2328	Qy Db
2327 599	AAGCAGGGATGGTACCTACCCGGCAGGTAGGTTAGATGTGGGTGG	2268 540	Qy Db
2267 539	TCGCCTTAAAAGAGCCCATTTCTTAGCTGCTGAAATCAGTGCTCTTTCACTTCTTCAGAG	· 2208	Qу Db
2207 479	TACCTTATTAACAGGAAATGCTAAGGTACCTTCTCTGTGGAACAATCTGCAATGTCTAAA	2148	Db Og
2147 419	CCCAGCCCAGAAAGGTGATTCTTCTCTTTACCATTTCTGGGGACTTTAGTCTTAATTAGG	2088 361	Qy dd
2087 360	TTTAGATGAAATAGAAGTTCAGGGTCCCTCACTCTAGTCACTAAAGAAGGATTTTACTCC	2028 301	Qy Db
2027 300	TIGTTTTTCATCCATATCCAAGTTCTGCAGACCACACAGGAACTTGCTTCATGGCTC	1968 241	Db Qy
1967 240	AGATAACTTTATTTTCTTCTTACTCCTTTCCTCTTGATTTTTTTCCTATAATTTCATTC	1908	p 09
180	TGGACCATACTACCAAGGACCAGTCCACCTGAACCACACTCTAAAGAAATATTTTTTA	121	망

Search completed: April 20, 2003, 16:28:38 Job time: 6549 secs

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16, Appl 2, Appl 3, Appl 4, Appl 1, Appl 1, Appl 15, Appl 16, Appl 17, Appl 17, Appl 18, Appl 19, Appl 11, Appl

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Minimum DB
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2: /cgn2_6/ptodata/1
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US-09-404-8798-40
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Sequence 26, Appl
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Sequence 1, Appl1
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Sequence 249, Appl
Sequence 14, Appl
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Query Match
Best Local Similarity 99.7
Matches 830; Conservative
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APPLICANT: Hillman
APPLICANT: Corley
                                                                                                                                                                                                                                           TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
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MEDIUM TYPE: Diskette
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                              TELEPHONE: 415-855-0555
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ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,7
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                                                                             LIBRARY: BLANCE 1519044
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APPLICANT: Shah, Purvi
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STATE: CA
COUNTRY: USA
ZIP: 94304
                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: single
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Corley, Neil C.
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US-08-194-088B-15

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US-08-194-087-15

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CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2226
TYPE: DNA
                                                             Patent No. 5376210
GENERAL INFORMATION:
APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 25885-1651
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PATENT DOCUMENT NUMBER: 08/896,005
PATENT POLLING DATE: 1997-07-17
PUBLICATION DATE: 1998-12-29
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LOCATION: (1)..(2226)
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          TCCACTCCCACCAGACTTGCTCATTTTTCGAGTTTTTAACTAGACTACACTCTATTTGAG
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APPLICANT: Lewis, Marcia E.

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS

FILE REFERENCE: CCD-257 (US)

CURRENT APPLICATION NUMBER: US/09/328,111

CURRENT FILING DATE: 1999-06-08

EARLIER APPLICATION NUMBER: US 60/088,801

EARLIER FILING DATE: 1998-06-10

NUMBER OF SEQ ID NOS: 850

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 850

LENGTH: 636
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Best Local Similarity
Matches 418; Conserv
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LOCATION: (1)...(636)
OTHER INFORMATION: n = A,T,C
-09-328-111-850
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APPLICANT: Bushnell, Steven E.
APPLICANT: Carroll III, Eddie
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GAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCA 1005
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                                                                                   TTGTGGAAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGC 1065
                                                                                                                                        GAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCA
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                                                                     TTGTGGAAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGC
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Derti, Adnan
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99.5%;
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Pred. No. 3.7e-96;
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RESULT 4 US-09-318-448-26 ; Sequence 26, A

Application US/09318448

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APPLICANT: Johnson, William G.

APPLICANT: Stenroos, Edward S.

TITLE OF INVENTION: METHODS FOR DIAGNOSING, PRITITLE OF INVENTION: DEVELOPMENTAL DISORDERS

FILE REFERENCE: 601-1-057

CURRENT APPLICATION NUMBER: US/09/318,448

CURRENT FILING DATE: 1999-05-25

NUMBER OF SEQ ID NOS: 46

SOFTWARE: Patentin Ver. 2.0

SEQ ID NO 26

LENGTH: 2211

TYPE: DNA
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Best Local Similarity 61.9%;
Matches 498; Conservative
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AGGCTGCCATGGAGGGCTATGAGGTGACCACCATGGATGAGGCCTGTCAGGAGGGCCAACA 858
                            AGGCCTGCATGGATGGGTTCAGGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATG
                                                            CTCTCAAAGCTCTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGC 1299
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Pred. No. 6.1e-72;
0; Mismatches 306;
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LENGTH: 2211
TYPE: DNA
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TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
FILE REFERENCE: 2585-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Human S-adenosylhomocysteine PUBLICATION INFORMATION: DATABASE ACCESSION NUMBER: M61831/GenBank
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   TTGGTGGGAAACAAGTGGTGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTGCTG
                                                                           ACTTGTACTGCTGCCGAGAATCCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGT 1179
                                                                                                                                                                                                                                                                                                     ATGGGGGAGACTTAACCCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCC
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                                      ACCTCTATGGCTGCCGGGAGTCCCTCATAGATGGCATCAAGCGGGCCACAGATGTGATGA
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US-09-404-879A-40
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US-09-404-879A-40/c
                                                                                                                                                                         US-09-103-840A-1/c
                                                                                                                  Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
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SOFTWARE: FastSEQ for
SEQ ID NO 40
LENGTH: 292
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APPLICANT:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C2
CURRENT APPLICATION NUMBER: US/09/404,879A
CURRENT FILING DATE: 1999-09-24
              APPLICANT: FRASER, Claire M. APPLICANT: VENTER, John C. TITLE OF INVENTION: DNA SEQUENCES.
                                                                                                  APPLICANT: FLEISCHMAN, Robert D.
                                                                                   APPLICANT:
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CURRENT FILING DATE: 1998-06-24
NUMBER OF SEO ID NOS: 2
SOFTWARE: Patentin Ver. 2.1
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Pred. No. 3e-50;
D; Mismatches 377;
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MOLECULE TYPE:
US-08-669-536-1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                       Matches 514;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
APPLICANT: MASUTA
APPLICANT: UEHARA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (703) 205-8050 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 12
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                1212
                                                                                                                                                                                                    1092
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                                                                                                                                   1152
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                                                                                                                                                                                                                                                                   1032 CACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACGTCAAT 1091
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                                                                                                                                                                                                                                     694
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                                   874
                                                                                                                                                                                                                                                                                                        634 AAATATACCAAGATGAAGGAAAGACTCGTCGGTGTTTCTGAGGAAACTACCACTGGAGTT 693
                                                                                                                                                                                                                                                                                                                                      CITY: FALLS CHURCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
ACCGARATCGACCCCATCTGTGCTCTGCAGGCCTGCATGGATGGGTTCAGGGTGGTAAAG 1331
                                                                GGTGAGGTAGGCAAGGGCTGCTGTGCTGCTCTCAAAGCTCTTGGAGCAATTGTCTACATT 1271
                                                                                                                                                                                                  GATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTGGAT 1151
                                                                                                                                                                                                                                    AAGAGGCTTTATCAGATGCAGGCTAATGGAACTTTGCTTTTCCCTGCTATTAATGTTAAT 753
                                                                                                  GGTCTCATGAGGGCTACTGATGTTATGATTGCCGGAAAGGTTGCCCCTTGTTGCTGGTTAT
                                                                                                                                   GGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGCTAT 1211
                                                                                                                                                                   GGAGATGTCGGCAAGGGTTGTGCTGCTGCCTTGAAACAAGCCGGTGCCCCGTGTGATTGTG
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PO BOX 747
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ilarity 56.1%;
Conservative
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ORGANISMS IN WHICH THE
S-ADENOSYLHOMOCYSTEINE
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                                                                                                                                                                                                                                                                                                                                                                       Score 227.4; DB 2;
pred. No. 2.3e-49;
0; Mismatches 391;
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HYDROLASE (
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US-08-930-894-1
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                                                                                                                           COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1054 ATCATGGTTGACCACATGAGGAAGATGAAGAACAATGCCATTGTTTGCAACATTGGTCAC
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                                           CLASSIFICATION: 800 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: DRAPER, John
APPLICANT: SKIPSEY, MATC
APPLICANT: WARNER, Simon
TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEIN HYDROLASE PROMOTER
TUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
APPLICATION NUMBER: PCT/GB96/00882 FILING DATE: 10-APR-1996
                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                            CITY: Washington
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                                                                                                        FILING DATE:
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LOCATION: 26..1483
OTHER INFORMATION:
US-08-930-894-1
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FILING DATE: 10-APR-1995
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 8.5%;
Best Local Similarity 55.9%;
Matches 496; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1016
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TOPOLOGY: linear
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     CGATACAAGCAGGATGTGCTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGCTTG
                                                                                                                                                                 GCTGAGGGCCGACTCATGAACCTTGGGTGTGCCACTGGTCACCCCAGCTTTGTCATGTCC
                                                                                                                                                                                                                                                                 ATCAAGCCCCAGACTGACCGGTGGGTCTTCCCTGAAACCAACACTGGTATAATTGTTCTT 1195
                                                                                                                                                                                                                                                                                                               GTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAA---ACGAGTTGTCCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATCATGCTGGACCACATGAGGAAGATGAAGAACAATGCCATTGTCTGCAACATTGGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGTGAGGTAGGCAAGGGCTGCTGTGCTCCTCAAAGCTCTTGGAGCAATTGTCTACATT | 1271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGCTAT | 1211
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                                                         TGCTCCTTCACCAACCAGGTGATTGCTCAGCTAGAGTTGTGGAATGAGAAAGGCAAGCGGC
                                                                                                          ATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATG---CACCCGAGGGG
                                                                                                                                                                                                             GCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTT - - - CCCACCTTTGTTCTGTCC
                                                                                                                                                                                                                                                                                                                                                                            TTTGACAACGAGATTGACATGCTAGGTTTGGAGACATACCCTGGCATCAAGAGAATCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                TCCAACACAGAAATCGATGTGACCAGCCTCCGCAC - - - TCCGGAGCTGACGTGGGAGCGA
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Pred. No. 1.5e-46;
0; Mismatches 379;
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RESULT 10
US-08-204-740-8
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 base -- '
TYPE".
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                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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NAME: NO. 5753432nan, Kevin
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION:
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                                                                                                                                                          580 ACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTG 639
195
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                           640 CTCTGATTTCACTCAGGAAACGTGCTCAGGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAG 699
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                                                                                                                                                                                                                                                                                                                         TYPE: nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
 CTGGCTGCCTGCACATGACCGTGGAGACGGCCGTCCTCATTGAGACCCTCGTCACCCTGG
                                                                                                                             ACATCGGCCTGCCTGGGGACGCAAGGCCCTGGACATTGCTGAGAACGAGATGCCGG 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       , Application US/08204740 5753432
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Methods for Identifying
Suppressor Elements and
Growth in Cancer Cells
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Pred. No. 1.5e-09;
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Genes Associated with Malignant
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                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6087745nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,3:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
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                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
TYPE: nucleic acid
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: Methods for Identifying Genetic
TITLE OF INVENTION: Suppressor Elements and Genes Associated with Malignant
TITLE OF INVENTION: Growth in Cancer Cells
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FILING DATE: 18-MAY-1998
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                              GGGCTCAGTGCCGGCTGGTCTGCTTAACATCTAC 794
                                                                                               CTCTGATTTCACTCAGGAAACGTGCTCAGGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAG 699
                                                                                                                                                                                                ACATCGGCCTGGCTGGGGACGCAAGGCCCTGGACATTGCTGAGAACGAGATGCCGG 134
                                                               CTGGCTGCCTGCACATGACCGTGGAGACGGCCGTCCTCATTGAGACCCTCGTCACCCT
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3. Wacker Drive, 32nd Floor
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                                                                                                                                                                                                                                                                             Score 72.6;
Pred. No. 1.
                                                                                                                                                                                                                                                                 Mismatches
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1.5e-09;
hes 89;
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US-09-081-395-8
                                                                                RESULT 13
                                                              US-09-416-833-8
             Sequence 8, Application US/09416833 Patent No. 6197521 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                      Matches 126;
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SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
TYPE: nucleic acid
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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APPLICANT:
                                                                                                                                                                                                   195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TORNEY/AGENT INCOMES NAME: NO. 6083746nan, Kevin E REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                       75
                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 312-913-000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 18-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LASSIFICATION:
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                                                                                                                                                                GGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTAC 794
                                                                                                                                                                                                  CTGGCTGCCTGCACATGACCGTGGAGACGGCCGTCCTCATTGAGACCCTCGTCACCCTGG
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                                                                                                                                   GTGCTGAGGTGCAGTGGTCCAGCTGCAACATCTTC
                                                                                                                                                                                                                                   ACATCGGCCTGGCTGGCGACGCAAGGCCCTGGACATTGCTGAGAACGAGATGCCGG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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Gudkov, Andrei
                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                             RESULT 14
                                                                                           PCT-US95-02521-8
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Best Local Similarity 58.1
Matches 126; Conservative
                                                          Sequence 8, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6197521nan, Kevin
NAME: NO. 6197521nan, Kevin
NAME: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                               APPLICANT:
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                                                                                                                                                                         760 GGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTAC 794
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SOFTWARE: PatentI
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10 S. Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      289 base pairs
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58.6%;
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Suppressor Elements and Genes Associated with
Growth in Cancer Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PC-DOS/MS-DOS
Methods for Identifying Suppressor Elements and Growth in Cancer Cells
                                                                            PC/TUS9502521
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Pred. No. 1.5e-09;
0; Mismatches 89
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                Genes Associated with Malignant
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US-08-204-740-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: PCT/US95/02521
                            CLASSIFICATION: 435
ATTORREY/AGENT INFORMATION:
NAME: No.. 5753432nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                            SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-715-1000
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Local Similarity 58.6%;
hes 126; Conservative
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ITLE OF INVENTION: Methods for Identifying
ITLE OF INVENTION: Suppressor Elements and
ITLE OF INVENTION: Growth in Cancer Cells
                                                                                                        APPLICATION NUMBER: US/08/204,740 FILING DATE: 04-MAR-1994 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        75
                                                                                                                                                                                                 COMPUTER: IBM PC compatible OPERATURG SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                               CITY: Chicago
STATE: Illinois
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                                                                                                                                                                                                                                         MEDIUM TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION:
                                                                                                                                                                                                                                                                                                                                               E: Allgretti & Witcoff, Ltd.
10 S. Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kazarov, Alexander
Mazo, Ilya
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SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                       Floppy disk
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                                93,354-C
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Pred. No. 1.
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Search completed: April 20, 2003, 18:17:48
Job time: 3273 secs
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Best Local Similarity
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TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE:
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                                                                                                         753 GCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTAC 794
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                     ATGCCAGGGTTGATGCGCATGCGGGAGATGTACTCAGCCTCCAAGCCACTGAAGGGTGCT
                                                                         GCCCTGGGTGCTGAGGCGCGGTGGTCCAGCTGCAACATCTTC 285
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ilarity 56.8%;
Conservative
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Pred. No. 1.9e-08;
0; Mismatches 96;
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Title:
Perfect score:
Sequence:
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Maximum DB seq length: 2000000000
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 nucleic search, using sw model
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Packfiles1.seq:*
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US-08-776-944-9

US-07-920-281C-25

US-08-466-277-25

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US-09-385-982-216
                                      US-09-385-982-362

US-09-385-982-457

US-09-385-982-29

US-09-385-982-29

US-09-397-787-237

US-09-328-111-432

US-09-149-476-22

US-08-322-742-14
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US-09-404-879A-40
US-08-236-427-12
US-09-328-111-798
US-09-227-357-66
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3, Appli
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                                                        US-08-896-005-2
Query Match 21.0
Best Local Similarity 99.0
Matches 773; Conservative
                                                  STRANGE TOPOLOGY:
IMMEDIATE SOURCE:
LIBRARY: BLADTUT04
TONE: 1519044
                                                                                                                                                     TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE: 2226 base pair
                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
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2226 base pairs

21.6%;

Score 553; DB 2; Pred. No. 1.4e-236; 0; Mismatches 2;

Length 2226; Indels

1;

1;

RESULT 1 US-08-896-005-2 Sequence 2, Applicati Patent NO. 5854023 GENERAL INFORMATION: APPLICANT: Hillma APPLICANT: Corley APPLICANT: Shah, ITILE OF INVENTION NUMBER OF SEQUENCE CORRESPONDENCE ADD ADDRESSEE: INCY STREET: 3174 PO CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94304 COMPUTER READABLE MEDIUM TYPE: DI COMPUTER: IBM C OPERATING SYSTEM SOTWARE: FISSES CURRENT APPLICATION NUMB FILING DATE: FI PRIOR APPLICATION NUMB APPLICATION NUMB FILING DATE: ATTORNEY/AGENT IN NAME: BILLINGS REGISTRATION NUMB REGIS		C 28 23 23 23 36 5 23 5 23	
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CCATION US/08896005 Ilman, Jennifer L. Ilman, Jennifer L. Irley, Neil C. I, Preeti IA, Purv I Porter Drive Alto INCOMPATIBLE STEM: DOS ASTEM: DOS INTORNATION: INFORMATION: INFORMATION: INFORMATION: INTORNATION: INTOR	ALIGNMENTS	4 US-09-385-982-312 4 US-09-385-982-312 4 US-09-385-982-319 4 US-09-328-111-816 4 US-09-328-111-782 6 5498694-3 4 US-09-123-912-96 4 US-09-123-912-96 4 US-09-123-97-74 1 US-08-695-720A-5 1 US-08-698-551-3 2 US-08-698-551-3 2 US-08-649-341A-3 2 US-08-649-341A-3 2 US-08-649-341A-3 2 US-08-633-901B-3 2 US-08-839-032A-3 2 US-08-839-032A-3 4 US-09-185-258C-3	
HYDROLASE		Sequence 3 Sequence 3 Sequence 9 Sequence 9 Sequence 7 Patent No. Sequence 7 Sequence 5 Sequence 3	-
		523, App 312, App 315, App 816, App 96, App 1782, App 1782, App 174, App 174, App 174, App 174, App 175, App 176, App 177, App 17	•

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                                                                                                                                                                 Sequence 3, Application Patent No. 6376210 GENERAL INFORMATION:
                                                                                  TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1995-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: PATENTIN Ver. 2.0
                                                                         SOFTWARE: |
                                                                                                                                                          APPLICANT: Yuan,
FEATURE: misc_feature LOCATION: (1)..(2226)
                                    ORGANISM: Homo sapiens
                                                  LENGTH: 2226
TYPE: DNA
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Best Local S
Matches 773
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TCCACTCCCACCAGACTTGCTCATTTTTCGAGTTTTTAACTAGACTACACTCTATT 775
                        TCCACTCCCACCAGACTTGCTCATTTTTCGAGTTTTTAACTAGACTACACTCTATT 2503
                                                 ATAATGAGCATGGCTTGTTAAGATCAGGAGGCCCACTTGGATTTATAGTATAGCCCCTTCC
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Pred. No. 1.4e-236;
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RESULT 3 US-09-328-111-850/c

US/09328111

Sequence 850, Appatent No. 62623 GENERAL INFORMATION:

APPLICANT:

Steinmann, Endege, Wilson

Kathleen

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                                                                     GENERAL INFORMATION:
APPLICANT: Mitcham,
APPLICANT: King, Gor
APPLICANT: Algate, F
                                                                                                                                                        Sequence 40, Application US/09404879A Patent No. 6468546
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NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 850
LENGTH: 636
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OTHER INFORMATION: n - A,T,C or 09-328-111-850
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APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
APPLICANT: King, Gordon E.
APPLICANT: Ring, Gordon E.
APPLICANT: Algate, Paul A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER.
FILE REFERENCE: 210121.462C2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(636)
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370; Conserv
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Burgess, Christopher
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                                                                                                                 Mitcham, Jennifer L.
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; TYPE: DNA
; ORGANISM: HOMO sapien
US-09-404-879A-40
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Patent No.
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Best Local Similarity
Matches 237; Conserv
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CURRENT FILING DATE: 1999-09-24
NUMBER OF SEQ ID NOS: 393
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            TELEFAX: (919)541-868
INFORMATION FOR SEQ ID NO:
                                            FILING DATE: 13-MAY-193
ATTORNEY/AGENT INFORMATION:
NAME: SPRUILL, W. MUTTAY
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: S-15
TELECOMMUNICATION INFORMATION:
TELEPHONE: (919)541-8615
                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Iwasaki, Genji
TITLE OF INVENTION: Herbicide Resistant Plants
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/061,644
FILING DATE: 13-MAY-1993
                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                   CLASSIFICATION: 435
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Volrath, Sandra
Volrath, Sain-Ichi
Kolzumi, Sain-Ichi
Tada, Sachiyo
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                               (919)541-8689
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100.0%; Pred. No. 4.8e-96;
rative 0; Mismatches 0;
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                                                                                S-19558/P1/CGC 1706/CIP
                                                                                                                                                                                                                                                                      Version #1.25
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; IMMEDIATE SOURCE: ; CLONE: pIGPDat.2 US-08-236-427-12
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                                                                     US-09-227-357-66/c
                                                                                                                                                                                     Query Match
Best Local S
Matches 25
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NUMBER OF SEQ ID NOS: 850

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 798
                         Sequence 66, Application US/09227357 Patent No. 6342581 GENERAL INFORMATION:
                                                                                                                                                                                                                                                          LENGTH: 632
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(632)
OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity
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APPLICANT: F1scher et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: US 60/088,801
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PPLICANT: Monahan, John E.

PPLICANT: Schlegel, Robert

ITLE OF INVENTION: NOVEL HUMAN GENES AND GENE

PILE REFERENCE: CCD-257 (US)
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HYPOTHETICAL: N
ANTI-SENSE: NO
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ORGANISM: Ara
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o. 6262
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25; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catino, Theodore J.
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ilarity 100.0%;
Conservative (
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III, Eddie
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Pred. No.
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Pred. No.
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. 0.085;
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0.03;
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NUMBER OF SEQ ID NO
SOFTWARE: PatentIn
SEQ ID NO 66
                                  EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEO ID NOS: 672
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE: PZ010P1
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FILING DATE: 1999-01-08
                                                                                                                                                                             APPLICATION NUMBER: 60 FILING DATE: 1997-09-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 1997-07-08
APPLICATION NUMBER: 60/052,732
FILING DATE: 1997-07-08
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                                                                                                                                        FILING DATE: 1997-09-
                                                                                                                                                                                                                 APPLICATION NUMBER: 60/
FILING DATE: 1997-08-18
                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                        APPLICATION NUMBER:
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PPLICATION NUMBER: 60/051,932
ILING DATE: 1997-07-08
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LING DATE: 1997-07-08
PLICATION NUMBER: 60/051,918
LING DATE: 1997-07-08
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LING DATE: 1997-08-18
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LING DATE: 1997-07-08
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LING DATE: 1997-07-08
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ORGANISM: Homo sapiens
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                                                   ; ORGANISM: human
US-09-262-773-209
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Best Local S
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Best Local Similarity
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SEQ ID NO 209
LENGTH: 2933
Query Match
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                                                                                                                                                          CURRENT ARPLICATIÓN NUMBER: US/09/262,773
CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
                                                                                                                                                                                                           TITLE OF INVENTION: CHROMOSOME 11-LINKED CORONARY HEART DISEASE TITLE OF INVENTION: SUSCEPTIBILITY GENE CHD1
FILE REFERENCE: Myr1ad 3
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APPLICANT: Hess, Mark A.
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CURRENT ETLING DATE: 1999-06-30
PRIOR APPLICATION NUMBER: US 60/091,315
PRIOR FILING DATE: 1998-06-30
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TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA BINDING PROTEIN (RBP-7)
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH SAID NUCLEIC ACID.
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                                                                                         TYPE: DNA
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ENGTH: 999
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0.085;
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0.079;
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                  Length 2933;
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SEQ ID NO 210
LENGTH: 23071
TYPE: DNA
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Best Local :
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TITLE OF INVENTION: A NUCLEIC ACID ENCODING A RETINOBLASTOMA
TITLE OF INVENTION: AND POLYMORPHIC MARKERS ASSOCIATED WITH
FILE REFERENCE: GENSET.031A
FILE REFERENCE: GENSET.031A
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CURRENT FILING DATE: 1999-03-04
NUMBER OF SEQ ID NOS: 210
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SOFTWARE: Patent.pm
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CURRENT FILING DATE: 1999-06-30
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APPLICANT: Hess, Mark A.
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            NAME/KEY: allele
LOCATION: 90842
                                                                                                                                      NAME/KEY: allele LOCATION: 72794
                                                                                                                                                                                    TYPE: DNA
ORGANISM: Homo sapiens
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OTHER INFORMATION: 99-1437-325
                                                                          NAME/KEY: allele
LOCATION: 88073
                                                                                                                        OTHER INFORMATION: 5-124-273 :
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                                                            OTHER INFORMATION: 5-127-261
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Pred. No.
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polymorphic
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ELATURE: NAME/KEY: allele LOCATION: 727717	NAME/KEY: allele LOCATION: 160031 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 150329 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 146345 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 146328 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 134374 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 134362 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 134134 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 108471 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 108308 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 108149 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 108106 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 106940 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 103806 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 99117 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 99098 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 97152 OTHER INFORMATION:	NAME/KEY: allele LOCATION: 97122 OTHER INFORMATION:	LOCATION: 93714 OTHER INFORMATION:
72817	5-148-352	5-145-24	5-143-101	5-143-84	5-140-361	5-140-348	5-140-120	5-136-174	5-135-357	5-135-198	5-135-155	5-133-375	5-131-395	5-130-276	5-130-257	5-129-144	99-1442-22	5-128-60
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PERATURE:
PERATURE:
LOCATION: 103783..103828
OTHER INFORMATION: polymorphic fragment 5-131-395 SEQ ID57
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LOCATION: 72771..72817
OTHER INFORMATION: polymorphic fragment 5-124-273 SEQ ID51
OTHER INFORMATION: polymorphic fragment 5-133-375 SEQ ID37
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                                                                                                                                                                                                                      NAME/KEY: allele
LOCATION: 103783..103828
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.OCATION: 97130..97177
DTHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID54
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JCCATION: 93690..93736
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JCCATION: 93690..93736
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                           PEATURE:
NAME/KEY: allele
OCATION: 106918.
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LOCATION: 99094.
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'RAME/KEY: allele
.CCATION: 99094..99140
.THER INFORMATION: polymorphic fragment 5-130-276 SEQ ID35
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OCATION: 97099..97145
WHER INFORMATION: polymorphic fragment 99-1442-224 SEQ ID71
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COCATION: 97099..97145
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THER INFORMATION: polymorphic fragment 5-127-261 SEQ ID31
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OCATION: 99075.
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OCATION: 99075.
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WHER INFORMATION: polymorphic fragment 5-129-144 SEQ ID33
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THER INFORMATION: complement polymorphic fragment 99-1437-325
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OCATION: 90819.
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THER INFORMATION: polymorphic fragment 5-130-257 SEQ ID55
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OCATION: 97130.
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THER INFORMATION: polymorphic fragment 5–127–261 SEQ ID52
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OCATION: 88050.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement polymorphic fragment 99-1437-325 SEQ ID70
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RESULT 12
US-08-776-944-9/c
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                                                                                                   TELEFAX: (703) 816-41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: allele
LOCATION: 108084..1
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2539 TGTCCAAAAAAAAAAAAAAAAAAA 2563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: polymorphic fragment 5-135-198 SEQ ID60
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OCATION: 108127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AME/KEY: allele
                                                                                                                                           TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 816-4006
                                                                                                                                                                                                                                   APPLICATION NUMBER: GB 9417211.1 FILING DATE: 25-AUG-1994 ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATION: 108127.
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CCATION: 106918
                                                                                      SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                           RIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: TULLY, (APPLICANT: SULLIVAN (ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ME/KEY: allele
CATION: 108084.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPLICANT: SULLIVAN, KEVIN
ITLE OF INVENTION: NUCLEOTIDE SEQUENCING METHOD
UMBER OF SEQUENCES: 19
                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/0 FILING DATE: 14-FEB-1997 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                 NAME: SCRAWFORD, ARTHUR R. REGISTRATION NUMBER: 25,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: U.S.A. ZIP: 22201-4714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ice 9, Apr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VIRGINIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/08776944
                                                                  56 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1100 NORTH GLEBE ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TULLY, GILLIAN
                                                                                                                                                                                                                                                                                                                                                                                      Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                        Floppy disk
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DNA (genomic)
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                                                                                                     3) 816-4100
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                                                                                                                                                                                 1498-92
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0.067;
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2541 TCCAAAAAAAAAAAAAAAAA 2563
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                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ANTI-SENSE:
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                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                             MOLECULE TYPE:
                                                                                                     ORIGINAL
                                                                                                                   ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UMBER OF SEQUENCES:
           LOCATION: 1.80
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                TELEPHONE: / 03 - 241 - 2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Birch, St
STREET: P.O. Box 747
CITY: Falls Church.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32 TCCAAAAAAAAAAAAAAAAAAAA 10
                                                                                                                                                                                      TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                     NAME: Murphy Jr., Gerald M
REGISTRATION NUMBER: 28,97
                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin palane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
les 23; Conserv
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                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                        NAME/KEY:
                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                           POPOLOGY:
                                                                                      RGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25
  INFORMATION:
                                                                                                    SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Virginia
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                                                                                      Semliki Forest Virus
                                                                                                                                                           linear
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                                                                                                                                              RNA
                                                                                                                                                                                                                                                                                                                                                                                13-AUG-1992
                                                                                                                                                                         single
                                                                                                                                           (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Expression Systems Based 
Alphaviruses
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Stewart,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0.9%;
/label= terminator
/note= "3' terminal sequence of cDNA expression
vector complementary to alphavirus genomic RNA"
                                                                                                                                                                                                                                                                                                                                                                                             US/07/920,281C
                                                                                                                                                                                                                                                                                                                  28,977
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                                                                                                                                                                                                                                                                                                         828-103P
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                                                                                                                                                                                                                                                                                                                                                                                                                         Version #1.25
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0.73;
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Matches Query Match Best Local

23; Conservative

0.9%;

s: Score 23; DB; Pred. No. 0.7

DB 1;

Length 80

Indels

0,

Gaps

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IOCATION: 1.80

OTHER INFORMATION: /label= terminator
/notte= "3' terminal sequence of cDNA expression
vector complementary to alphavirus genomic RNA*

SEQUENCE DESCRIPTION: SEQ ID NO: 25:
US-08-466-277-25'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-466-277-25
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                                                                              Query Match Best Local Similarity Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEX: 248345
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
                   2541 TCCARARARARARARARARARA 2563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/920,281
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: MUIPHY JT., Gerald M.
REGISTRATION NUMBER: 28 977
REFERENCE/DOCKET NUMBER: 828-103P
TELECHMUNICATION INFORMATION:
TELEPHONE: 703-241-1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: DNA Expression Systems Based on
                                                                                                                                                                                                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                        ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Garoff, Henrik
Liljestrom, Peter
                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear MOLECULE TYPE: RNA (9)
TCCAAAAAAAAAAAAAAAAAAA 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 80 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/466,277
FILING DATE: 06-Jun-1995
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                            SENSE: NO
                                                                                                                                                                                                                                                                                                                                     ORGANISM: Semliki Forest Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 703-241-2848
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPONDENCE ADDRESS:
ADDRESSE: Birch
STREET: P.O. Box 747
ZITY: Falls Church
                                                                              0.9%; Score 23; DB 4; ilarity 100.0%; Pred. No. 0.72; Conservative 0; Mismatches
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                                                                                  0
                                                                                                                       Length 80
                                                                                  Indels
                                                                                  0;
                                                                                  Gaps
                                                                                  0
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RESULT 15 US-09-385-982-187/c

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EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILLING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILLING DATE: 1998-08-31
NUMBER OF SEO ID NOS: 544
SOFTWARE: FastSEO for Windows Version 3.0
SEO ID NO 187
LENGTH: 256
                                                        Query Match
Best Local Similarity
Tatches 23; Conserve
                                                                                                                                                     ; FEATURE:
, NAME/KEY: misc_feature
; LOCATION: (1)...(256)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-187
  밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:

APPLICANT: ENDECE, WILSON O., ET AL.

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION

TITLE OF INVENTION: PRODUCTS: II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 187, Application US/09385982
                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
EARLIER APPLICATION NUMBER: 09/328,111
EARLIER FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILE REFERENCE: CCDNA-260XX
                                                                                                                                                                                                                                                   TYPE: DNA ORGANISM: Homo sapiens
                                      2541 TCCAAAAAAAAAAAAAAAAAAA 2563
  33
TCCAAAAAAAAAAAAAAAAAAA 11
                                                                            Conservative
                                                                                             0.9%;
                                                                          0;
                                                                                               Score 23;
Pred. No.
                                                                            Mismatches
                                                                                               DB 4;
0.68;
                                                                                                                   Length 256;
                                                                              Indels
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Search completed: April 20, 2003, 21:12:54
Job time : 185 secs

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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Word size
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Searched:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Title:
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                                                                                                                                                                                                                                                                              000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq length: 0
seq length: 2000000000
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2563
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22.2
14.4
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'Ggn2_6/ptcdata/1/pubpna/US08_PUBCOMB.seq:*
'Ggn2_6/ptcdata/1/pubpna/US09_NEW_PUB.seq:*
'Cgn2_6/ptcdata/1/pubpna/US09_PUBCOMB.seq:*
'Cgn2_6/ptcdata/1/pubpna/US10_NEW_PUB.seq:*
'Cgn2_6/ptcdata/1/pubpna/US10_PUBCOMB.seq:*
'Cgn2_6/ptcdata/1/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq
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  10 US-09-880-107-346
10 US-09-783-590-278
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10 US-09-847-519A-1
10 US-09-887-576-15
10 US-09-783-590-4696
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10 US-09-783-590-4696
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US-09-884-441-40

US-09-867-701-2023

US-10-021-121-1

US-09-880-107-346
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Sequence 1, Appli
Sequence 439, App
Sequence 1031, Ap
Sequence 1031, Ap
Sequence 2023, Ap
Sequence 203, Appli
Sequence 346, Appl
Sequence 278, Appl
Sequence 261, Appl
Sequence 161, Appli
Sequence 178, Appli
Sequence 178, Appli
Sequence 178, Appli
Sequence 179, Appli
Sequence 1474, Ap
Sequence 1474, Ap
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US-09-867-550-1185	US-10-001-887-12	US-09-834-975-947	US-09-525-978B-74	US-09-864-864-161	US-09-864-864-126	US-09-834-975-619	US-09-777-564-855	US-10-015-219-855	us-09-867-701-9355	US-09-867-701-8988	US-09-983-965-3122	US-09-768-827-7	US-09-867-701-8875	US-10-274-974-3	US-09-764-870-622	US-10-125-540-622	US-09-764-870-98	US-10-125-540-98	US-10-012-452-1	US-09-938-842A-5235	US-09-983-802-66	US-09-770-149-438	US-09-879-536-798	US-09-925-301-43	us-09-867-701-10512
e 11	Sequence 12, Appl	e 94	Sequence 74, Appl	16	Sequence 126, App	61	e 85	855	Sequence 9355, Ap	,8868	Sequence 3122, A	Sequence 7, Appli	Sequence 8875, Ap	Sequence 3, Appli	Sequence 622, App	•	Sequence 98, Appl	Sequence 98, Appl	Sequence 1, Appl		66,	438,	79	Sequence 43, App.	Sequence 10512, A
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ປS-09-782-051-1
                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Hart, Derek N J
                                                                                                                                                                                                        Matches 2563;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/782,051
CURRENT FILING DATE: 2001-02-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Enzyme having S-adenosyl-L-homocysteine hydrolase TITLE OF INVENTION: (AHCY) type activity FILE REFERENCE: 24305 MRB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: NZ 299507 PRIOR FILING DATE: 1996-10-04
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2563
TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
121 CGCAGCTCGACGCAGGGGCCGGCAGGAGGGTGGGCGATCGCGTGTCGGAGGGCGCCGCGC
                                                             61 GTCCGGCTGCCTTGGGCCTGCCGAACAGACAAGGCCGTGGGCCACAGCACCTCAGAAGCCGA 120
                                                                                                                                              1 GGCGCGGGCAGGTCGGAGCTCGGAGCTGCTGCTTCTGGTTCTCTTGTGGCCACCGTCGCT
                                      GTCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCAGAAGCCGA 120
                                                                                                                       GGCGCGGGCAGGTCGGAGCTCGGAGCTGCTTCTGGTTCTCTTGTGGCCACCGTCCCT 60
                                                                                                                                                                                                        Conservative
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Pred. No. 0;
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; LOCATION: (688)
; OTHER INFORMATION: n equals a,t,g, or US-09-925-300-439
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CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO 439
LENGTH: 721
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APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic Acids, Proteins and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                           FEATURE:
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                                                                                   CGCTGGCCGGCCGGGGAATGTCGATGCCTGACGCGATGCCCGCTGCCCGGGGTCGG
                                                                                                                                            GAAGCCGACGCAGCTCGACGCAGGGGGCCGGCAGGAGGGTGGGCGATCGCGTGTCGGAGGG
                                                                                                                                                                                                                      CCGTCGCTGTCCGGCTGCCTTGGGGCTGCCGAACAAGGCGTGGGCCACAGCACCTCA 115
                                                                                                                                GAAGCCGACGCACGCACGCACGCCACGCCACGACGGTGGCCCATCGCGTGTCGCACGG
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                                                               GGAGGAGCTGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGGCCAC
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                                                                                                                                                                                                                                                                            a 22.28;
Similarity 99.88;
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20020151681A1
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                           Score 570; DB 10;
Pred. No. 1.5e-292;
                                                                                                                                                                                                                                                                    Mismatches
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NAME/KEY: misc_feature
LOCATION: (1)...(636)
OTHER INFORMATION: n =
US-09-879-536-850
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 850
LENGTH: 636
                                                                                                                                                                                                Matches
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Best Local :
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CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/088,801
PRIOR FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: NOVEL HUMAN GENES AND TITLE OF INVENTION: PRODUCTS FILE REFERENCE: CCD-257 (US)
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                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                          756 CTGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAAACTCAAATGAAGTAGCT 815
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                                                                    GCAGCACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGGCGAGTCAGAAGATGAC
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                                                                                                                         CTGGGGGCTCAGTGCCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCT 311
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                                                 GCAGCACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGGCGAGTCAGAAGATGAC
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370; Conserv
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Catino, Theodore J.
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Bushnell, Steven E.
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Monahan, John E.
Schlegel, Robert
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                                                                                                                                                                                             14.4%; Score 370; DB 10;
100.0%; Pred. No. 3.6e-186;
tive 0; Mismatches 0;
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GATGATGGGGGAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAG 995

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PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1031
LENGTH: 376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-880-107-1031/c
; Sequence 1031, Application US/09880107
; Patent No. US20020142981A1
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US-09-880-107-1031
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Horne, Darci T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: DNA
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              2474 TTCGAGTTTTTAACTAGACTACACTCTATT 2503
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76
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                                                                                                                GTAGGTTAGATGTGGGTGGTGCATGTTAATTTCCCTTTAGAAGTTCCAAGCCCTGTTTCCT 197
                                                         GGAGGCCCACTTGGATTTATAGTATAGCCCTTCCTCCACTCCCACAGACTTGCTCATTT 77
                                                                                                                                                                                                         GTAGGTTAGATGTGGGTGCATGTTAATTTCCCTTAGAAGTTCCAAGCCCTGTTTCCT 2353
                                                                                                                                                                                                                                       TACCTTCTCTGTGGAACAATCTGCAATGTCTAAATCGCCTTAAAAGAGCCCATTTCTTAG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GCTGGGAAGCTCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTT 11
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TTCGAGTTTTTAACTAGACTACACTCTATT
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Scherf, Uwe
Gene Logic, Inc.
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47
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                                                                                                                       ; NAME/KEY: misc_feature
; LOCATION: (1)...(553)
; OTHER INFORMATION: n = A,T,C or
US-09-867-701-2023
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                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NO SOFTWARE: FastSEQ 1 SEQ ID NO 2023
LENGTH: 553
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LENGTH: 292
TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Carter, Darrick
APPLICANT: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462C7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2023, Appli patent No. US2002013 GENERAL INFORMATION:
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Best Local Similarity
Matches 237; Conserv
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                                                                                Query Match
                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSEQ for Windows Version
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CURRENT FILING DATE: 2001-06-18
                                                                                                                                                                                                             TYPE: DNA ORGANISM: Homo sapien
                                                                                                                                                                                                 FEATURE:
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1322 GGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAA 1381
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Sim hes 224;
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                                                                Similarity
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0020132237A1
                                                Conservative
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                                              Score 224; DB 10;
Pred. No. 1.6e-108;
0; Mismatches 0;
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                                                                                  Length 553;
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; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-021-121-1
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Patent No. US20020142444A1
GENERAL INFORMATION:
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SEQUENCE CHARACTERISTICS:
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FILING DATE: 19-Max-1996
ATTORNEY/AGENT INFORMATION:
NAME: TOICHIA, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDITOM TYPE: 3.5 inch, 1.44 Mb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                             FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic Factor
NUMBER OF SEQUENCES: 10
                                                                                                                                                            FEATURE
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                                                                                                                                                                                                                   NAME/KEY:
                                                                                                                   NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 1877 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
TOPOLOGY: Linear
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FILING DATE: 06-Dec-2001
CLASSIFICATION: <Unknown>
                                                                             IDENTIFICATION METHOD: OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                      NAME/KEY:
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                                                                                                                                                                                                IDENTIFICATION METHOD:
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244-321
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    Score 190;
    DB 12;
Length 1877;
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LENGTH: 384
TYPE: DNA
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                                                        GENERAL INFORMATION:
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                                                                        Patent No. US20020110850A1
                                                                                             Sequence 278, Application US/09783590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-00 CURRENT APPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14
                  APPLICANT:
                                      APPLICANT: Dillon, Patrick J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/211,379 PRIOR FILING DATE: 2000-06-14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100 nes 168; Conservative
                                                                                                                                                                                              GGGAAACAAGTGGTGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGC 240
                                                                                                                                                                                                                                    GGGAAACAAGTGGTGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGC 1232
                                                                                                                                                                                                                                                                          TACTGCTGCCGAGAATCCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGTTTGGT 192
                                                                                                                                                                                                                                                                                                                                                       CTCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATGTAGTGACACGGGA 1327
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCACTTGGATCGCATGAAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACACACAGA 1267
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Scherf, Uwe
Gene Logic, Inc.
Haseltine, William A.
Li, Haodong
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Pred. No.
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; Mismatches
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                                                                      ; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-114-893-33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 1.8%;
Best Local Similarity 100.0%;
Matches 45; Conservative
                  Best Local Similarity
                                    Query Match
                                                                                                                                          SEQ ID NO 33
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LENGTH: 140
   Matches
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NUMBER OF SEQ ID NOS: 12485
SOFTWARE: Patentin Ver. 2.0
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CURRENT EILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
                                                                                                                                                                             NUMBER OF SEQ ID NOS: 321
                                                                                                                                                                                              EARLIER APPLICATION NUMBER: 09/413,232
EARLIER FIGING DATE: 1999-10-06
                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/114,893
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TILE OF INVENTION: Human Genes, Sequences, and Expression Products 16.2
TLE REFERENCE: PO-16.2C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc feature
COCATION: (71)
THER INFORMATION: n equals a,t,g, or
NAME/KEY: misc feature
COCATION: (117)
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(GANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ence 33, Application US/10114893 ication No. US20020193567A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HER INFORMATION: n equals a,t,g,
                                                                                                                                                                                                                                                                  LICANT: Kelleher, Kerry S.
LICANT: Genetics Institute, Inc.
LE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
E REFERENCE: GI 6000-10A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
   26;
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                                                                                                                                                                                                                                                                                                                                   Bowman, Michael R.
Spaulding, Vikki
Carlin-Duckett, McKeough
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Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kenneth
                                                                                                                                                                                                                                                                                                                                                                                                                David
                    1.0%; Score 26; DB 9;
100.0%; Pred. No. 0.003
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                    0.0034;
 0; Indels
                                   Length 863;
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US-09-847-519A-1
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                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                         Sequence 1, Application US/09847519A Patent No. US20020102693A1
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                                          APPLICANT: We1, BO
TITLE OF INVENTION: DSP-14 DUAL-SPECIFICITY PHOSPHATASE
FILE REFERENCE: 200125.422
CURRENT APPLICATION NUMBER: US/09/847,519A
CURRENT FILING DATE: 2001-05-01
NUMBER OF SEQ ID NOS: 17
                                                                                                                             APPLICANT: Luche, APPLICANT: We1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/770,445
CURRENT FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: US 60/178,472
PRIOR FILING DATE: 2000-01-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(987)
OTHER INFORMATION: n = A,T,C or G
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TYPE: DNA
ORGANISM: Arabidopsis thaliana
FEATURE:
LENGTH: 1165
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                              PatentIn
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Hurban, Patrick
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Ledford, Brooke L.
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Price, Jennifer L.
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~aka, Joshua G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Yong-Qiang
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100.0%; Pred. No.
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; ORGANISM: Homo sapiens
US-09-847-519A-1
                      FILE REFERENCE: 1360.001US1

CURRENT APPLICATION NUMBER: US/09/887,576

CURRENT FILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: US 60/213,848

PRIOR FILING DATE: 2000-06-23

PRIOR APPLICATION NUMBER: US 60/214,087

PRIOR FILING DATE: 2000-06-23

PRIOR PILING DATE: 2000-06-23

PRIOR PILING DATE: 2000-06-23

PRIOR PILING DATE: 2000-12-29

PRIOR FILING DATE: 2000-12-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 3304, Application US/09938842A Patent No. US20020160378A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION UNMBER: US 60/264,647
PRIOR FILING DATE: 2001-01-16
PRIOR FILING DATE: 2001-01-16
                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Budworth, P.
                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: US 60/300,111 PRIOR FILING DATE: 2001-06-22
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URRENT APPLICATION NUMBER: US/09/938,842A
URRENT FILING DATE: 2001-08-24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Harper, Jeff
APPLICANT: Kreps, Joel
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LICANT: Zhu, Tong
LE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING
LE OF INVENTION: SAME, AND METHODS OF USE
                                                                                                                                                                                                                          LICANT: Cooper, Bret Le OF INVENTION: Promoters for regulation of plant expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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Chang, H.
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)S: 5379 .
Windows Version 4.0
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100.0%; Pred. No.
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0.0034;
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0.0035;
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Search completed: April 20, 2003, 23:52:52

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; SEQ ID NO 15;
LENGTH: 2003;
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-887-576-15
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                             β
                                                                                                                                  ; OTHER INFORMATION: n equals a,t,g, or c US-09-783-590-4696
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US-09-783-590-4696
                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 1
SOFTWARE: PatentIn Ver.
SEQ ID NO 4696
LENGTH: 101
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Best Local Similarity

Matches 26; Conserv
                                                                Best Local
Matches
                                                                                 Query Match
Best Local :
                                                                                                                                                                           NAME/KEY: misc feature
LOCATION: (10)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
LOCATION: (89)
OTHER INFORMATION: n equals a,t,g, or c
NAME/KEY: misc feature
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                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: 08/420,856
PRIOR FILING DATE: 1995-04-12
PRIOR APPLICATION NUMBER: 08/346,731
PRIOR FILING DATE: 1994-11-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/09/783,590
CURRENT FILING DATE: 2000-02-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IITLE OF INVENTION: Human Genes, Sequences, and Expression Products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLICANT: Dillon, Patrick J.
                                                                                                                                                                                                                                                                                                       FEATURE:
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25; Conserv
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                                                                 Conservative
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Pred. No. 0.0035;
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Title: Perfect score: Sequence:

US-09-782-051-1 2563

Scoring table:

Searched:

Word size

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45

em_estba:*

em_esthum:* ≥m_estmu: estin:

Run

April 20,

OM nucleic -

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Total number of hits satisfying chosen parameters:
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
Location/Qualifiers
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Full-length cDMA libraries and normalization
Unpublished (2001)
contact: Genoscope
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Mammalia; Eutheria;
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/clone="CSODC027YC19"
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sapiens cDNA clone CSODC027YC19 5
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em_gss_hum:* em_gss_inv:* em_estom:* em_estfun:

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Qy 309 GCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGGCCACCGTCACCAAGGCGCCC	Qy 249 GGGGAATGTCGATGCCTGACGCGATGCCGCTGCCCGGGGTCGGGGAGGAGCTGAAGCAG	Qy 189 GGGCGGGCCCAGAGGGGGAAAGAGGCGGGGGGGGGGGG	OY 129 GACGCAGGGCCGGCAGGAGGTGGGCGATCGCGTGTCGGAGGGCGCCGCGGGCAGGC	Oy 69 GCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCAGAAGCCGACGCAGCTC	Query Match 32.7%; Score 837; DE Best Local Similarity 99.9%; Pred. No. 0; Matches 887; Conservative 0; Mismatches	AL551097 AL5	Oy 1189 A 1189 Db 901 A 901.
TTCATGGCCACCGTCACCAAGGCGCCC 368	CCCGGGGTCGGGGAGGAGCTGAAGCAG 308 	GGCGGGTCAGCCGCTGGCCGGGCCGGC 248 	GTGTCGGAGGGCGCCGCGCGGGCAGGC 188	ACAGCACCTCAGAAGCCGACGCAGCTC 128	; DB 9; Length 921; 0; ches 1; Indels 0; Gaps 0;	ITI_NFL006_PL2 Homo sapiens cDNA clone CSODIO66YN07 5 INA sequence. I GI:12888715 I Grubber,C., Jesse,J. and Polayes;D. Cloneli, Primates; Catarrhini; Hominidae; Homo. Cloneli, Primates; Catarrhini; Hominidae; Homo. Cloneli, Primates; Catarrhini; Hominidae; Homo. Controlonalides and normalization Genoscope - Centre National de Sequencage O6 EVRY cedex - France Genoscope.cns.fr, Web: www.genoscope.cns.fr. Genoscope.cns.fr. Genoscope.cns.fr, Web: www.genoscope.cns.fr. Genoscope.cns.fr. Web: www.genoscope.cns.fr. Genoscope.cns.fr. Ge	AGENCAL CONTRACT OF TRACES AND ACCOUNTS AND

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                                                                                                                                    Volor10, S., Simon, G., Repetto, M., C., G., Ballablo, A. and Zollo, M. Sequencing analysis of forty-eight to drosophila mutant protein DNA Seq. 9 (5-6), 307-315 (1998)
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                                                                                     Gontact: Zollo, Massimo
Selethon Institute of Genetics and
Via olgettina 58, Milan, MI 20132,
Email: zollo@tigem.it.
                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1379)
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/clone-"239
/clone_lib="Soares infant brain
/sex="female"
/dev_stage="73 days post natal"
                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
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Location/Qualifiers
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Tissue Procurement: ATCC/DCTD/DTP
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_1lb="NIH_MGC_72"
/clone_1lb="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pcWV-SPORT6; Site_1: Noti;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo
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BQ212518
BQ212518.1 GI:20392818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
Eukaryota; Metazoa;
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AGENCOURT_7595081 NIH_MGC_72 Homo sapiens cDNA clone
                                                                                                                                                                                                                                                                                                                                               Tissue Procurement: ATCC/DCTD/DTP
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D
                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mammalia;
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                                                                                                                                                                                                                    quality sequence stop:
           /clone_lib="NIH_MGC_72"
//tissue_type="melanotic melanoma"
//tissue_type="melanotic melanoma"
//lab_host="melloß (phage-resistant)"
//note="Organ: skin; Vector: pCMV-SPORT6; Si
Site_2: Sali; Cloned unidirectionally. Pri
Average insert size 2 kb. Library constru
Technologies"
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                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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L1,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
                                           Mammalia; Eutheria;
1 (bases 1 to 858)
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    CTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGAAGAGAG
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BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
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                                                                                AGGGTGGTAAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGA 1379
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Plate: LLCM2070 row: j column:
High quality sequence stop: 688.
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cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Ammmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1021)

NIH-MCC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
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/lab_host="NH10B (phage-resistant)"
/note="Organ: lymph; Vector: prompt; Site_1: XhoI; Site_2:
/note="Organ: lymph; Vector: prompt; Site_1: XhoI; Site_2:
/note="Organ: lymph; Vector: prompt; Site_1: XhoI; Site_2:
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AGENCOURT_6400881 NIH_MGC_67
5', mRNA sequence.
PM4.04.7
                                                                                                                                                     Onpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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                 High quality sequence stop: 694.
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/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by
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Plate: LLCM2608 row: d column:
High quality sequence stop: 700.
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bloscience Corporation
Clone distribution: MGC clone distribution information car
found through the I.M.A.G.E. Consortium/LLNL at:
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National Institutes of Health, Mammalian Gene Collection
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/lab_host="Philos (phage resistant)"
/lab_host="Philos (phage resistant)"
/note="Organ: lung: Vector: pOTB7; Site_1: EcoRI; Site_2:
XhoI; cDNA made by oligo-dr priming. Directionally cloned
into EcoRI/XhoI sites using the following 5 adaptor:
GGCACGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
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Mammalia; Eutheri
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NIH-MGC http://mg/
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue procurement: ATCC/DCTD/DTP
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Contact: Robert Strausberg, Ph.D.
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                                                                                                                                             /clone="IMAGE:5578170"
/clone_lib="NIH_MGC_72"
/tissue_type="melanotic melanoma"
/lab_host="DH1OB (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: |
Site_2: Sall; Cloned unidirectionally. Primer: O
Average insert size 2 kb. Library constructed b;
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Institutes of Health, Mammalian Gene Collection
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/db_xref="taxon:9606"
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                       HRI human cDNA project Unpublished (2000) Contact: Takao Isogai
                                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 745)
                                                                                            Ota, T., Nishikawa, T.,
 Helix Research Institute
               Genomics Laboratory
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u,A., Nakamura,Y., Nagai,T., Sugano,S
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Catarrhini;
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1; Hominidae; Homo.
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Tel: 81-438-52-3975
Fax: 81-438-52-3986
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cells after 2-weeks retinoic acid (RA) induction"
149 c 214 g 186 t 3 others
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/db_xref="taxon:9606"
/clone="NT2RP3003545"
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GGGCGATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGC 1736	TGTCCATCACAGCCACAACAGAGCTTTGGCACTGATAGAACTCTATAATGCACCCGAG 319	CTGTCCATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCGGAG 1676	GTCCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACATTTCCCACCTTTGTT 259	FOCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTT 1616	ACGTGGGAGCGAGTACGTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTT 199	CGTGGGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTT 1556		GCAATATGGGCCACTCCAACACAGAAATCGATGTGACCAGCCTCCGGCACTCCGGAGCTG 1496	GGAAATAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTA 1436 	ch 26.4%; Score 676; DB 13; Length 1059; il Similarity 100.0%; Pred. No. 0; 676; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	S77 Catarrhini; Vertebrat primates; Craniata; Vertebrat primates; Catarrhini; Hominic claim, 1, 1, 1, 1, 1, 2, 2, 1, 1, 1, 1, 2, 2, 1, 1, 1, 1, 2, 2, 1, 1, 1, 1, 2, 2, 1, 1, 1, 2, 2, 1, 1, 1, 2, 2, 1, 1, 1, 2, 2, 1, 1, 1, 2, 2, 1, 1, 1, 2, 2, 1, 1, 1, 2, 2, 1, 1, 1, 1, 2, 2, 1, 1, 1, 1, 2, 2, 1, 1, 1, 1, 1, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	BM547143 1059 bp mRNA linear EST 20-FEB-2002 AGENCOURT_6499536 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5730185

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Genoscope - Centre National de Se
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, i
                                                                                                                                                                                                                                                                                                                                                                                                         Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)
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                                                                                 was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMySpORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com"
                                                                                                                                                                                                                     /note-"Organ:
                                                                                                                                                                                                                                    /tissue_type="neuroblastoma cells"
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                                                                                                                                                                                                                                                              /sex="male"
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/db_xref="taxon:9606"
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tissue Procurement: Miklos Palkovits, M.D., Ph.D. cDNA Library Preparation: Michael J. Brownstein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plate: LLAM13577 row: a column: High quality sequence stop: 656.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 933)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLA DNA Sequencing by: Agencourt Blosclence Corporation Clone distribution: MGC clone distribution information
                     231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              through the I.M.A.G.E. Consortium/LLNL at:
                                                            5'-GACTAGTTCTAGATCGCGAGCGGCCGCCT(15)-3'. Size selected > 1 kb for average insert length 1.7 kb. This is a primary library non-amplified. Library constructed by Life Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor College of Medicine) and is available through Life
                                         Technologies.
                                                                                                                                                                  /note-"Vector: pCMV-SPORT6 (Life Technologies); Silvoti; Site_2: Sall; cDNA made by oligo-dT priming: Directionally cloned using the following adaptors: 5'-TCGACCCACGCGTCCG-3' and
                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6185747"
                                                                                                                                                                                                                                                  /tissue_type="dorsal root ganglia"
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                      /clone_lib="Lupski_dorsal_root_ganglion"
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Query Match
Best Local Similarity
Matches 656; Conserv

25.6%; Score 656; 100.0%; Pred. No.

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Length 933; Indels

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Mismatches

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Search completed: April 20, Job time: 3278 secs 2003, 22:06:43

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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                                        GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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2 US-09-746-660A-101
US-09-758-853A-4
US-10-037-598-26
US-09-738-626-838
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Sequence 2023, App
Sequence 850, App
Sequence 217, App
Sequence 314, App
Sequence 1031, App
Sequence 1031, App
Sequence 40, Appl
Sequence 4, Appl
Sequence 97, Appl
Sequence 97, Appl
Sequence 1, Appl
Sequence 101, App
Sequence 4, Appl1
Sequence 26, Appl
Sequence 838, App
Sequence 4421, Ap
Sequence 11499, A
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	Sequence 2035, Ap	Sequence 8, Appli	5161,	Sequence 278, App	679,	12043		838, 7	7284,				Sequence 117, App	e 1007	837	Sequence 9, Appli	Sequence 7006, Ap	Sequence 12928, A	Sequence 2191, Ap	ence 1179, Ap	ence 1179, Ap	ence 1179, Ap	ence 1179, Ap	Sequence 9160, Ap		Sequence 1423, Ap

ALIGNMENTS

	C 180	QY 121 CGCAGCTCGACGCAGGGGCCGGCAGGAGGGTGGGCGATCGCGTGTCGGAGGGCGCCGCGC
	A 120	61
	A 120	QY 61 GTCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCAGAAGCCGA
	60	Db 1 GGCGCGGGCAGGTCGGAGCTGCTGCTGCTTCTGTTGTTGTGGCCACCGTCGCT
	- ii	Qy 1 GGCGCGGGCAGGTCGGAGCTCGGAGCTGCTTCTGGTTCTCTTGTGGCCACCGTCGCT
0	Gaps	Best Local Similarity 100.0%; Pred. No. 0; Matches 2563; Conservative 0; Mismatches 0; Indels 0;
		100 OP: Goog Sand: DB 10: Toggth
		US-09-782-051-1
		INFORMATION:
	5	ORMATION: Open reading frame extends without a
		: LOCATION: (3)(1847)
		; ORGANISM: Homo sapiens
		; SOFTWARE: Patentin Ver. 2.1
		FILING DATE: 1996-10-04
		FILING DATE: 1997-1
		CURRENT APPLICATION NUMBER: US/09/782,051
		; TITLE OF INVENTION: (AHCY) type activity
	ase	S,
		; APPLICANT: Hart, Derek N J
		GENERAL INFORMATION:
		; bequence I, Application US/09/82051
		US-09-782-051-1
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APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 439
LENGTH: 721
                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Nucleic Acids, Proteins and FILE REFERENCE: PA101 CURRENT APPLICATION NUMBER: US/09/925,300 CURRENT FILING DATE: 2001-08-10 PRIOR APPLICATION NUMBER: PCT/US00/05988 PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1890
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                 NAME/REY: misc feature
LOCATION: (688)
OTHER INFORMATION: n equals a,t,g, or c
)9-925-300-439
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                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
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            TGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGGCCACCGTCACCA
                                                                                                    CGCAGCTCGACGCAGGGGCCGGCAGGAGGGCGATCGCGTGTCGGAGGGCGCCGCGC 180
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TGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGGCCACCGTCACCA
                                                   GGGCCGGCCGGGGAATGTCGATGCCTGACGCGATGCCGGCTCCCGGGGTCGGGGAGGAGC
                                                                            GGGCCGGCGGGAATGTCGATGCCTGACGCGATGCCGCTGCCCGGGGTCGGGGAGGAGC
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                                                                                                                                                                                                                                                                                                                            27.4%;
98.0%;
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Pred. No. 2.2e-189;
6; Mismatches 8;
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, NAME/KEY: misc_feature
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CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2023
IENGTH: 553
TYPE: DNA
ORGANISM: Homo sapien
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Best Local :
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Matches 541;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER FILE REFERENCE: 210121.497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan
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nilarity 97.5%;
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Pred. No. 1.1e-129;
D; Mismatches 9;
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US-09-879-536-850/c
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; LOCATION: (1)...(636)
; OTHER INFORMATION: n = A,T,C
US-09-879-536-850
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TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/879,536
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/088,801
PRIOR APPLICATION NUMBER: US 60/088,801
PRIOR FILING DATE: 1998-06-10
NUMBER OF SED ID NOS: 850
SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 850
LENGTH: 636
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Best Local Similarity
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                                                                            AGTGCCGCTGGTCTGCTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG
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Catino, Theodore J.
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Monahan, John E.
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SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 217

LENGTH: 2200

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
FEATURE:
NAME/KEY: misc_feature
LOCATION: (2188)
OTHER INFORMATION: n equals a,t,g, or
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APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
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Best Local Similarity
Matches 745; Conserv
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PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
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CURRENT FILING DATE: 2001-08-10
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US-10-044-090-344
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Sequence 344, Application US/10044090
Patent No. US20020137081A1
GENERAL INFORMATION:
APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090
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; ORGANISM: Homo sapiens FEATURE: NAME/KEY: misc_feature; OTHER INFORMATION: Incyte US-10-044-090-344
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NUMBER OF SEQ ID NOS: 8
SOFTWARE: PERL Program
SEQ ID NO 344
LENGTH: 2429
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Best Local Similarity
Matches 745; Conser
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AAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACACAGAAATCGATGTGACCAGCC 1479
                                                                                                                                             AGGCCTGCATGGATGGGTTCAGGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGÄTG
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                                        TCTTTGTCACCACCAGGCTGTATTGACATCATCCTTGGCCGGCACTTTGAGCAGATGA 947
                                                                              TCGTAATAACTTGCACAGGAAATAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGA 1419
                                                                                                                   AGGCTGCCATGGAGGGCTATGAGGTGACCACCATGGATGAGGCCTGTCAGGAGGGCAACA 887
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Pred. No. 4.2e-104;
0; M1smatches 525;
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SOFTWARE: PatentIn Ver.
SEQ ID NO 1031
LENGTH: 376
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Best Local Similarity
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PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer FILE REFERENCE: 44921-5028-WO CURRENT EPPLICATION NUMBER: US/09/880,107 CURRENT FILING DATE: 2001-06-14
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                                                                                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
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Scherf, Uwe
Gene Logic, Inc.
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Pred. No. 1.5e-93;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 346
LENGTH: 384
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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Best Local Similarity
Matches 381; Conserv
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PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PatentIn Ver. 2.1
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TITLE OF INVENTION: Gene Expression Profiles
FILE REFERENCE: 44921-5028-WO
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                    TGTGCTCTGCAGGCCTGCATGGATGGGTTCAGGGTGGT-AAAGCTAAATGAAGTCATCCG
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TGTGCTCTGCAGGCCTGCATGGATGGGTTCAGGGTGGTAAAAGCTAAATGAAGTCATCCG
                                                                  CCTGTGCTGCTCTCAAAAGCTCTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATC
                                                                                       -CTGTGCTGCTCTC-AAAGCTCTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATC
                                                                                                                                                                          TGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTG 1231
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Conservative
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Pred. No. 1.4e-85;
0; Mismatches 0
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US-09-884-441-40/c
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US-09-759-990-1
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Matches 273; Conservation
                                                                                                                                                                                                                                                                   Sequence 1, Application US/09759990
Patent No. US20020119491A1
GENERAL INFORMATION:
APPLICANT: AntiCancer, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 489
SOFTWARE: FASTSEQ for Windows Version
SEQ ID NO 40
LENGTH: 292
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                                             SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 1
                                                                                               APPLICANT: Han, Oinghong
TITLE OF INVENTION: HIGH EXPRESSION AND PRODUCTION OF HIGH
TITLE OF INVENTION: SPECIFIC ACTIVITY RECOMBINANT S-ADENOSYLHOMOCYSTAINASE
TITLE OF ENVENTION: (SAHH) AND IMPROVED ASSAYS FOR S-ADENOSYLMETHIONINE (SA
FILE REFERÊNCE: 31276-20026.00
CURRENT APPLICATION NUMBER: US/09/759,990
CURRENT FILING DATE: 2001-01-12
PRIOR APPLICATION NUMBER: US 60/176,444
PRIOR FILING DATE: 2000-01-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Algate, Paul A.
APPLICANT: Carter, Darrick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.463C7
CURRENT APPLICATION NUMBER: US/09/884,441
CURRENT FILING DATE: 2001-06-18
                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                        APPLICANT:
                 TYPE: DNA
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ORGANISM: Homo sapien
ORGANISM: Unknown
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Pred. No. 3.9e
0; Mismatches
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Best Local Similarity
Matches 493; Conserv
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                                                                                                                                                                                     ATGGATGAATACGTTGCCAGCTTGCATCTGCCATCATTTGATGCCCACCTTACAGAGCTG 1775
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TACCGTTATTAA 1461
                                      TACAGATACTAA 1847
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                                                                               ACACAGAAGCAGGCTGACTACATCAACGTTCCAGTTGAGGGTCCTTACAAGTCTGATGCT
                                                                                                                     ACAGATGACCAAGCAAAATATCTGGGACTCAACAAAAATGGGCCCATTCAAACCTAATTAT 1835
                                                                                                                                                            CTCGATGAAGAAGTCGCTCGCCTCCACCTCGGATCTCTCGATGTCCACCTTACAAAGCTT 1389
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Pred. No. 1e-58;
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RESULT 11 US-09-746-660A-97 ; Sequence 97, Application US/09746660A ; Publication No. US20030049804A1

ENERAL INFORMATION:

CANT: Pompejus, Markus

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Qy 1011 GAAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGT 1070
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Best Local Similarity
Matches 482; Conserv
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LOCATION: (101)..(1534)
OTHER INFORMATION: RXN00132
-09-746-660A-97
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IITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
IITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Corynebacterium glutamicum
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APPLICATION NUMBER: 60/141031
PTITING DATE: 1999-66-25
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R OF SEQ ID NOS:
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ATCGTATGCAATATGGGCCACTCCAACACAGAAATCGATGTG---ACCAGCCTCCGCACT 1487
                                            GCGACCGGCAACAAGGACATCATTTCCTTCGAGCAGATGCTCAAGATGAAGGATCACGCT
                                                                                                                                                                                        GATGGGTTCAGGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACT 1370
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                                                                                         TGCACAGGAAATAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGT 1430
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Zelder, Oskar
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Pred. No. 6.9e-55;
0; Mismatches 354;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 1557;
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; ORGANISM: Corynebacterium glutamicum
US-09-738-626-836
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US-09-738-626-836
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                                                                                                                     SEQ ID NO 836
LENGTH: 1422
TYPE: DNA
                    Query Match
Best Local Similarity
    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 836, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROS
                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                    NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                       PRIOR FILING DATE:
                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                    ITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ILE REFERENCE: 249-125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1725 TACGTTGCCAGCTTGCCATCTGCCATCATTTGATGCCCACCTTACAGAGCTGACAGATGAC 1784
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1415 AAGGTGGCACGCATCCACGTTGAGGCTCTCGGCGGTCAGCTCACCGAACTGACCAAGGAG 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1358 CA---AAACGAAGGACAGTACGAGAACGAGGTCTACCGTCTGCCTAAGGTTCTCGACGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1238 CGCTCCATCATCGTCCTGTCCGAAGGTCGCCTGTTGAACCTTGGCAACGCCACCGGACAC
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                                                                                                                                                                                                                                         APPLICATION NUMBER: JP 00/280988
    477;
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                                                                                                                                                                                 PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                          YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
IKEDA, MASATO
                                                                                                                                                                                                                                                                                                                                                                                                                       OZAKI, AKIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OCHIAI, KEIKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HAYASHI, MIKIRO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Application US/09738626

o. US20020197605A1
    Conservative
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                                                                                                                                                                                                                     2000-08-03
                  56.84;
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    0
                    Score 225.6; DB 9 Pred. No. 1.7e-53;
  Mismatches
                                       DB 9;
    354;
  Indels
                                       Length
                                         1422;
9;
Gaps
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1011 GAAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGT 1070

GAGGAAACCACCACCGGTGTGCACCGCCTGTACCACTTCGCTGAAGAAGGCGTGCTGCCT

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RESULT 13
US-10-021-121-1/c
US-10-021-121-1/c
; Sequence 1, Application US/10021121
; Patent No. US200201424441
; GENERAL INFORMATION:
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                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                         APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neurotrophic
NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                  STATE: California
                                                                                                                                                                                                         CITY: South San Francisco
                                                                                                                                      ZIP: 94080
                                                                                                                                                           COUNTRY:
            SOFTWARE: WinPatin (Genentech)
                                                                                                                                                             USA
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                                                                                                                                                                                                                                   US-09-746-660A-101
; Sequence 101, Application US/09746660A
; Publication No. US20030049804A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                            APPLICANT:
                                                                                                                                                             APPLICANT:
                                                                                                                                                                                       APPLICANT:
                                                                                     APPLICANT:
                                                                                                                                      APPLICANT:
                                                                                                                                                                                                            APPLICANT: Pompejus, Markus
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SEQUENCE CHARACTERISTICS:
LENGTH: 1877 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                 1266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1446 CCCCATCTGTGCTCTGCAGGCCTGCATGGATGGGTTCAGGGTGGTAAAGCTAAATGAAGT 1387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1283 CCCCATCTGTGCTCTGCAGGCCTGCATGGATGGGTTCAGGGTGGTAAAGCTAAATGAAGT 1342
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APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
CLASSIFICATION: <Unknown>
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NAME: TOICHIE, PhD., Timothy
REGISTRATION NUMBER: 36,700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE
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TELEPHONE: 650/225-8674
TELEPAX: 650/952-9881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AATCGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AATCGATGTG 1472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACACAGA 1267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACAGA 1462
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: Nucleic Acid
Kim, Jun-Won
Lee, Heung-Schick
Hwang, Byung-Joon
VENTION: CORYNEBACTERIUM GLUTAMICUM.GENES ENCODING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: signal peptide 
LOCATION: 244-321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Transmembra
LOCATION: 901-978
IDENTIFICATION METHOD:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS: Double
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                                                                                                                                                             Schroder,
                                                                                                          Haberhauer, Gregor
                                                                                                                                 Zelder, Oskar
                                                                                                                                                                                  Kroger, Burkhard
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Conservative (
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901-978
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LOCATION: (101)..(1396)
OTHER INFORMATION: FRXA
US-09-746-660A-101
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Best Local :
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SEQ ID NO 101
LENGTH: 1396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 09/606740
PRIOR FILING DATE: 2000-06-23
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1396
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                           1371
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Local Similarity 57.3%;
Les 377; Conservative
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FILING DATE: 2000-03-09
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    CGCTCCATCATCGTCCTGTCCGAAGGTCGCCTGTTGAACCTTTGGCAACGCCACCGGACAC
                                                                                                                                                                  CTGCTGGGCAACATCGGTCACTTTGATAATGAGATCGATATGCATTCCCTGTTGCACCGC
                                                                                                                                                                                                  ATCGTATGCAATATGGGCCACTCCAACACAGAAATCGATGTGACCAGCCTC---CGCACT 1487
                                                                                                                                                                                                                                                   GCGACCGGCAACAAGGACATCATTTCCTTCGAGCAGGATGCTCAAGATGAAGGATCACGCT 1117
                                                                                 GACGACGTCACCCGCACCACGATCAAGCCACAGGTCGACGAGTTCACCTTCTCCACCGGT
                                                                                                                         CCGGAGCTGACGTGGGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGC
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                                        AAACGAGTTGTCCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCC
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Pred. No. 3.2e-42;
0; Mismatches 275;
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; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 318013_region_A3
US-09-754-853A-4
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Best Local S
Matches 428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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TITLE OF INVENTION: Nucleic Acid Molecules And Other Molecules Associated With
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/174,880 PRIOR FILING DATE: 2000-01-07 NUMBER OF SEQ ID NOS: 1119
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CATCAAGCCCCAAACTGACAGATGGGTCTTCCCTGAGACCAACACCGGTATCATTGTCTT
                                      AGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTC---CTCCT
                                                                                                                                                                                                                   AGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCA | 1450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TGGTCTCATGAGGGCTACCGATGTTATGATTGCTGGAAAGGTGGCTGTTGTGGCTGGATA 178859
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                                                                                   CTTTGACAATGAGATCGACATGCTTGGGCTGGAGAACTACCCCGGCGTGAAGCGCATCAC | 17855
                                                                                                                                                                                                                                                              CTTGGAGGATGTTGTTGTGAGGCTGATATCTTTGTCACCACCGGTAACAAGGACAT
                                                                                                                                                                                                                                                                                                    GCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATGT | 1390
                                                                                                                                                                                                                                                                                                                                                   GACCGAGATTGATCCCATCTGTGCCCTTCAGGCTCTCATGGAAGGCCTTCAGGTTCTGAC
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428; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55,48;
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Pred. No. 9.6e-38;
0; Mismatches 333;
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178499
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Page 11

Qy 1565 GGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACC---TITGTTCTGTC 1621
b 178498 GGCTGAGGGTCGATTGATGAACTTGGGATGCGCCACTGGACACCCCAGTTTTGTGATGTC 178439 Db 178258 CAGTGTGCCTGTTGAGGGTCCATACAAGCCTGCTCACTACAGGTACTAAGTGA 178206 1799 GGGACTCAACAAAAATGGGCCATTCAAACCTAATTATTACAGATACTAATGGA 1851

Search completed: April 20, 2003, 19:29:31
Job time: 1363 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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35041 6	BI33504	1	\sim	27.4	02.	4
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59448 6	BG25944	:		.7	03.	ï
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89173 A	BQ88917	Ľ	w	8	20.	8
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94873 A	BQ89487	7	N	8	24.	4
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ALIGNMENTS

		source	FEATURES		COMMENT	MEDLINE	JOURNAL		TITLE		AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	LOCUS	U69200
-	/organism="Homo sapiens" /db_xref="taxon:9606" /map="1p13.3" /clone="23931"	11379	Email: zolio@tigem.it. Location/Qualifiers	Via Olgettina 58, Milan, MI 20132, Italy	Contact: Zolio, Massimo	99452388	DNA Seq. 9 (5-6), 307-315 (1998)	to drosophila mutant protein	Sequencing analysis of forty-eight human image cDNA clone's similar	,G., Ballabio,A. and Zollo,M.	Volorio, S., Simon, G., Repetto, M., Cucciardi, M., Banfi, S., Borsani	1 (bases 1 to 1379)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	human.	BST.	U69200.1 GI:2739423	U69200	sequence.	U69200 Soares infant brain 1NIB Homo sapiens cDNA clone 23931, mRNA	U69200 1379 bp mRNA linear EST 27	
									s similar		Borsani		•	eostomi;							3931, mRNA	EST 27-OCT-1999	

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Query Match 51.5
Best Local Similarity 99.1
Matches 1349; Conservative
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AK014539.1
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                                                             Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K. Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Normalization and subtraction of cap-trapper-selected cDNAs prepare full-length cDNA libraries for rapid discovery of negenome Res. 10 (10), 1617-1630.(2000)
                                                                                                                                                                           Carninci, P. and Hayashizaki, Y. High-efficiency full-length cDNA Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                           clone:4631427C17.
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itoh,M., Aizawa,K.,
kiyama,J., Nishi;K.,
                                                                                                                                                                                                                                   Chordata;
Rodentia;
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Sciurognathi; Muridae
Nagaoka, S., Sasaki, N., C
Kitsunai, T., Tashiro, H.,
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mouse cD
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Carninci, P., ., Itoh, M.,
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(S. Adachi, J., Alzawa, K., Akahira, S., Akimura, T., Aono, H., Arai, A., Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Rawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Kurihara, C., Matsuyama, T., Okazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Salto, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schriml, L., Shibata, K., Shibata, Y., Shinagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
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prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGATCCAAGAGCTCTTTTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5']
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fax:81-45-503-9216)
Please visit our web site (http://genome.gsc.riken.go.jp/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Ranagawa 230-0045, Japan (E-mail:genome-resegsc.riken.go.jp,
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/strain="C57BL/6J"
/db_xref="FANTON_DB:4631427C17"
/db_xref="MGD:MGI:1907499"
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OY 1557 GTCCTCCTGGCACAGGGTCTACTCAATTTGACCTGCTCACAGTTTCCCACCTTTGTT 1616 11	20 GGAAATAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGAAAACAGTTGTATCGTA 1437 TGCAATATGGGCCACCCAACACACACAAAAACAGTTGTATCGTA 111111111111111111111111111111111111	normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics seconstructed by C. Gruber (Invitrogen). Research Genetics secons tracking code 012." SE COUNT 290 a 242 c 221 g 304 t 2 others roll of the construction	High quality sequence stop: 747. FEATURES 1. 1059 1. 1059 20	AUTHORS NIH-MGC http://mgc.nci.nih.gov/. AUTHORS NIH-MGC http://mgc.nci.nih.gov/. TITLE National Institutes of Health, Mammalian Gene Collection (MGC) JOURNAL Unpublished (1999) COMMENT Email: cgapbs-remail.nih.gov Tissue Procurement: Invitrogen cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAML728 row: k column: 18	BM547143 AGENCOURT 5', mRNA s BM547143 BM547143.1 EST. human

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AL527928
                                                                       L1, W.B., Gruber, C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
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                                                                                                                                                       Mimmalia; Eutheria;
1 (bases 1 to 938)
                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
映mmalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                       Homo sapiens
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111: segref@genoscope.cns.fr,
                                                                                                                                                                                                                                                                                     mRNA sequence.
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/organism="Homo sapiens"
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Local Similarity 99.7%;
hes 936; Conservative
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                                                                                                            TTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGAG
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                                              ACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTG
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was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pchySPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: filang@lifetech.com URL: http://fulllength.invitrogen.com" /db_xref="taxon:9606" /clone="CSODC027YC19" /clone_1ib="LTI_NFL003_NBC3" /note-"Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA /lab_host*"DH10B" /sex-"male" /tissue_type="neuroblastoma cells" Score 926.2; DB 9; Pred. No. 1.3e-157; 2; Mismatches 0; Length 938;

Indels

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Gaps

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         GGGGGAATGTCGATGCCTGACGCGATGCCGCCTGCCCGGGGTCGGGGAGGAGCTGAAGCAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segref@genoscope.cns.fr, Web : www
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Genoscope
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 921)
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AL551097 LTI_NFL006_PL2
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                                                                                                                                                                                                                                                                                                                 /tissue_type="placenta"
/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
/note="Vector: pcMVSPORT 6; Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pcMVSPORT 6
vector. Library was normalized. Library was constructed by
Life Technologies. Contact: Feng Liang Life Technologies,
a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
Email: filiang@lifetech.com URL:
http://fulllength.invitrogen.com"
1 others
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/clone_lib="LTI_NFL006_PL2"
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/db_xref="taxon:9606"
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Pred. No. 2.1e-152;
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                                                                                        Mammalia; Eutheria; Primates; 1 (bases 1 to 957)
Li,W.B., Gruber,C., Jessee,J.
Full-length cDNA libraries and Unpublished (2001)
                                                                                                                                                                                                                                      prime, mRNA
AL520703
AL520703.1
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segræf@genoscope.cns.fr, Web : www
Location/Qualifiers
1. .957
                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/db_xref-"taxon:9606"
/clone-"CSODB002YL22"
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l; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrefégenoscope.cns.fr, Web : www
Location/Qualifiers
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AL527927
AL527927.1 GI:12791420
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http://fulllength.invitrogen.com"

177 c 223 g 255 t 4 others
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/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="CSODC027YC19"
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization unpublished (2001)
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/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
/mote="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of Invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"
94 a 238 c 299 g 158 t 2 others
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AL574762 AL574762 LTI_NFL006_PL2 prime, mRNA sequence. AL574762 AL574762.1 GI:12935277 EST. human: Homo sapiens Eukaryota; Metazoa; Chc Mammalia; Eutheria; Pri 1 (bases 1 to 916) Li,W.B., Gruber, C., Jes Full-length cDNA 11brar Unpublished (2001) Contact: Genoscope Genoscope - Centre Nati BP 191 9106 EVRY cedex Email: seqref@genoscope Email: seqref@genoscope Location/Quali e	ACACTCTATT 2503 ACAGTCTATT 9	AGTATAGCCCTTCCACTCCACCAGACTTGCTCATTTTTCGAGTTTTTAACTAGACT	GTTCAGAGATGTGTATAATGAGCATGGCTTGTTAAGATCAGGAGGCCCAC 	GCATGTTAATTTCCCTTAGAAGTTCCAAGCCCTGTTTCCTGCGTAAAGGTGGTATG 	ACTTOTTCAGAGAAGCAGGGATGGTACCCTACCCGGCAGGTAGGT	GCAATGTCTAAATCGCCTTAAAAGAGCCCATTTCTTAGCTGCTGAAATCAGTGC 	TAGTCTTAATTAGGTACCTTATTAACAGGAAATGCTAAGGTACCTTCTC	AAGGATTTTACTCCCCAGCCCAGAAAGGTGATTCTTCTCTTTTACCATTTCTGGGGAC 	GCTTCATGGCTCTTTAGA:	PATAATTTCATTCTTGTTT	AGAAATATTTTTAAGATAA(ATTACAGATACTAATGGACCATACTACCAAGGACCAGTCCACCTGAACCACACACTC 	AGATGACCAAGCAAAA
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y Match Local Similarity 96.9%; Pred. No. 3.9e-146; hes 908; Conservative 0; Mismatches 25; Indels 4; Gaps 3 532 AGAAGCAGCAAACCCAAGGGCAGCAGCAGTTTCTGTGTGAAGAACATCAAGCAGG 591	High quality sequence stop Incation/Qualifie 1.1042 /organism="Homo s /db_xref="taxon:9 /clone="IMAGE:549 /clone_lib="NHLM /tissue_type="Tet /hab_host="DH10B /note="Organ: eye Site_2: Sali; Clo Average insert si Technologies." 267 a 219 c 309	BM449470 AGENCOURT 5', mRNA BM49470 BM449470 BM449470 EST human 4 Homo sapi Eukaryota Eukaryota Mammalla; 1 (bases NIH-McC National Unpublish Contact: Email: cg Tisue pr cDNA Lib DNA Sequ	ATGTTAATTTCCCTTAGAAGTTCCAAGCCCTGTTTCCTGCGTAAAGGTGGTATGTCCAGT

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L1,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: segrefgenoscope.cns.fr, Web: www.gen
                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 865)
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/db_xref="taxon:9606"
/clone="CSODB004YI04"
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/lab_host="DH10B"
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Pred. No. 6e-145;
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Tissue Procurement: ATCC/DCTD/DTP
CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC Clone distribution informati
found through the I.M.A.G.E. Consortium/LLNL at;
http://lmage.llnl.gov
plate: LLAM12332 row: m column: 19
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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BM468564
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Location/Qualifiers
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/db_xref="taxon:9606"
/dlone="IMAGE:579170"
/clone_lib="NH_MGC_72"
/tlssue_type="melanotic melanoma"
/tlssue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/lab_host="Organ: skin; Vector: pcMV-SPORT6; Site_1: NC_Site_2: Sali; Cloned unidirectionally. Primer: Ol: Average insert size 2 kb. Library constructed by Technologies."
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Email: seqref@genoscope.cns. Location/Qualiflers e 1. 858	ee, J. and Polayes, D. es and normalization nal de Sequencage - France	AL554850.1 GI:12896025 EST. human Homo sapiens Fuktoroote. Metazoa: Chordata: Crandata. Vertabrata. Futeloo	AL55485 AL55485 Prime,	TGTGAACATGGATGGGTGGCAGGCCAACATGATĆCTGGATGATGGGGGAGACT 951	CAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTG 898	CTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGGCTGAGGCTGGAGTTG 840 	CCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGTCGTCTG 780	GTGCTCAGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACACACAC	GACGCCGGGAGATIGAGATIGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAA¢ 660 	AAACCAACTCCAAGGGCAGCAATTTCTGTGTGAAGAACATCAAGCAGGCAG	GTTCAGCTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGC 540 	CCAAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACA 480	AGGCGCCCAAGAAGCAAATCCAGTTTGCTGATGACATGCAGGAGTTCACCAAATTCCCCA 420 	TGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGGCCACCGTCACCA 360 	GGGCCGGCGGGGAATGTCGATGCCTGACGCGATGCCCGCTGCCCGGGGTCGGGGAAGGAA	GGGCAGGCGGGCGCGCCAGAGGGGGAAAGAGGCGGGGGGG

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                                                       AACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGA 1012
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/fissue_type="placenta"
/fisue_type="placenta"
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/db_xref="taxon:9606"
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3; Mismatches 0;
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TITLE
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Matches 949; Conserv
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                                                                               AGGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGA
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Plate: LLCM2070 row: j column: 22
High quality sequence stop: 688.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC http://mgc.nc1.n1h.gov/.
National Institutes of Health, Mammalian Gene Collection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostom1; Mammalia; Eutheria; Primates; Catarrhin1; Hominidae; Homo.

1 (bases 1 to 1021)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA sequence.
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a 245 c
                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pOTB7; Site_1: XhoI; Site_2:
ECORI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GCCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
ILRT (Life Technologies). Note: this is a NIH_MGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="IMAGE:5815413"
/clone_lib="NIH_MGC_99"
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/db_xref="taxon:9606"
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Search completed: April Job time : 3309 secs

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10595.712 Million cell updates/sec
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                                                                                                                                                                                                                                                                                           /gcgdata/geneseq/geneseqn-embl/NA1999.DAT:
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                                                                            AAV28617
AAV73924
ABV23195
     ABV29032
AAS76216
ABV44141
AAZ80766
ABV35309
ABV14215
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Human SAHH DNA #1.

Human prostate exp
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Human prostate exp
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Human prostate exp
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  Hart DNJ;
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                                                  04-OCT-1996;
                                                                                                     09-APR-1998
                                                                                                                           WO9814562-A1
                                                                                                                                                                                                                                                                                                                                             AAV28617;
                                                                                                                                                                                                                                                                                                                                                                     AAV28617 standard; cDNA; 2563 BP
                           (HART/) HART D
                                                                           06-OCT-1997;
                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                        Nucleotide sequence of the ODD4b5.3 enzyme
                                                                                                                                                                                                                                                                                                                   21-AUG-1998 (first entry)
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101.8
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3..1847
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AAS96121
ABK52394
AAH68526
AAH65802
AAC46817
AAT44513
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AAC91228
AAC77823
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AAI61373
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C glutamicum codin C glutamicum codin Arabidopsis thalia Asparagus S-adenos Arabidopsis thalia Arabidopsis thalia Arabidopsis thalia

C. glutamicum gene SahH gene encoding

Nicotiana tabacum S-adenosylhomocyst Ripening banana pu Fusarium venenatum Soybean 318013 reg Corynebacterium gl C. glutamicum gene Corynebacterium gl

Zea mays DNA fragm Drosophila melanog DNA sequence upstr Genomic fragment # Moraxella catarrha

Human prostate exp Human prostate exp Aspergillus oryzae Drosophila melanog

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This is the nucleotide sequence of the DD4b9.3 enzyme which has S-adenosyl-L-homocysteine hydrolase (AHCY)-type activity. Its products can be used to identify substances which have a stimulatory
                                                                         S-adenosyl-5-homocysteine hydrolase; SAHH; human; treatment; infection; cancer; autoimmune disease; gene mapping; antisense; therapy; antagonist; imm
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or inhibitory effect on the enzyme activity. Such substances can be used to modulate dendritic cell (DC) function and for immunomodulation. They can be used in the treatment of e.g. autoimmune diseases transplantations or cancers. The products can also be used for
                                                                                                                                 Human SAHH DNA #1.
                                                                                                                                                             04-MAR-1999
                                                                                                                                                                                        AAV73924;
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P-PSDB; AAW56097.
                                                Homo sapiens
                                                                                                                                                                                                                  AAV73924 standard; DNA;
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                                                                                                                                                                                                                                                                                      889
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                                                                                                                                                                                                                                                                                   TIGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGG 417
                                                                                                                                                                                                                                                                                                                                        AGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGA 360
                                                                                                                                                                                                                                                                                                                                                                                            GCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                            (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis.
         Location/Qualifiers 56..1558
                                                                                                                                                            entry)
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Pred. No. 2.2e-1
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                                                                                        drug screening;
detection; diagnosis;
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Best Local Similarity
Matches 417; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 3616 BP; 1017 A; 782 C; 826 G; 991 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence encodes a human S-adenosyl-5-homocysteine hydrolase The SAHH protein can be used to generate specific antibodies and screening to identify specific binding agents. Antagonists of the protein are used to treat or prevent a wide range of viral, bacte protein are used to treat or prevent a wide range of viral, bacte protein are used to treat or prevent a wide range of viral.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding human S-adenosyi-5-homocysteine hydrolase for production of recombinant enzyme, useful for diagnosis, treatment and prevention of cancers, infections and autoimmune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JUL-1997;
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                                                                                                                                                                                                                                                                                                         61 AGGCAGAATTTTGGACGCCGGGAGAATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 120
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DB; AAW90061.
                                  AGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTA 360
                                                                     GCCGCTGGTCTGCTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTG
                                                                                       GCCGCTGGTCTGCTAACATCTACTCAACTCAGATGAAGTAGCTGCAGCACTGGCTG
                                                                                                                                       CACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTTGGGGGGCTCAGT
                                                                                                                                                                                                            CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA
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 AGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTA
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                        Score 417; DB 20;
Pred. No. 2.6e-121;
Mismatches 0;
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Best Local S
Matches 417
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(e) selecting a composition for inhibiting prostate cancer in a patient (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; and determining whether prostate cancer in a
                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                    Sequence 3634
                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, used for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Schlegel
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-MAR-2000;
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                                                                                                                                                                                                                                                          (d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MILL-)
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AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 120
                                              GAGAGAAGCAGCAAACCAACTCCAAGGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGC 60
                                                                                                 al Similarity
417; Conserv
                                                                                                                                                                                                                                                                                                                                                                          ۲,
                                                                                                                                                                      also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                         in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         prostate
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                                                                                                                                                                                                                                                                                                                                                                         Page 4168-4169; 11750pp;
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                                                                                                 Conservative
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2000US-211314P.
2000US-219007P.
2000US-255281P.
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2000US-189862P.
                                                                                                                                                  BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            marker;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cytostatic;
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Pred. No. 2.6e-121; Mismatches 0;
                                                                                                                                                869
                                                                                                                                                                                                                                                                                                                                                                         English.
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                                                                                                                                                                                                indolence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carcinogen;
                                                                                                                                                  918
                                                                                                                                                  T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pharmacodyanamic
                                                                                                                                                                                                prostate cancer in a
                                                                                                                       Length
                                                                                                Indels
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                                                                                                Gaps
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RESULT 4
ABV29032
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a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:
(a) assessing whether a pattent is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
                                                                                                                                                               Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, used for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-SEP-2002
                                                                                                         The invention relates to an isolated nucleic acid molecule (I) a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) o
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate pharmacogenomic
                                                                                                                                            Claim
                                                                                                                                                                                                                                         Schlegel
                                                                                                                                                                                                                                                                                                                                              17-FEB-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                    WO200160860-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ABV29032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ABV29032
                                                                                                                                                                                                                                                                                                                                                                      20-FEB-2001; 2001WO-US05171
                                                                                                                                                                                                                                                               (MILL-) MILLENNIUM
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                                                                                                                                         Page 6147-6148; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                   2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-211907P.
2000US-255281P.
                                                                                                                                                                                                                                        Endege
                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer; marker;
                                                                                                                                                                                                                                                               PREDICTIVE MEDICINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDNA;
                                                                                                                                                                                                                                        Ŷ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                cytostatic;
gene; ss.
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  inhibiting prostate cancer in a patient; carcinogenic potential of a compound;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           carcinogen; pharmacodyanamic
                                                                                                         of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1015
                                    cancer
                                                                                                                                                                 state of
useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             marker;
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genetic disorders or other traits and to assess

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AAS76216/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
Matches 417; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        patient; (I) is a
New isolated polynucleotide and encoded polypeptides, diagnostics, forensics, gene mapping, identification (
                                                                                                                                                                                                                                                                                                                          Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic (
                                                                                                                                                                                                                                                                                                                                                                          DNA encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAS76216 standard; cDNA; 5030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 3634 BP;
                                                                                          Drmanac RT,
                                                                                                                                                                                                  30-MAR-2001; 2001WO-US08631
                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                       31-MAR-2000; 2000US-0540217
23-AUG-2000; 2000US-0649167
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                                              P-PSDB; ABG12029
                                                                                                                          (HYSE-) HYSEQ INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    determining whether prostate cancer has metastasized in a patient, assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        is also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 120
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                                                                                        Liu C,
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                                                                                                                                                                                                                                                                                                                                                                          human diagnostic protein #12020
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Pred. No. 2.6e-121;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                           forensic;
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                in
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                                                                                                                                                                              ABV44141/c
                                                                                                                                                                                                     RESULT 6
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and to produce other types of data and products dependent on DNA and amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention. Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIF at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences (I) is useful as hybridisation probes, polymerase chain reaction (PCR) primers, oligomers, and for chromosome and gene mapping, and in recombinant production of (II). The polynucleotides are also used in diagnostics as expressed sequence tags for identifying expressed genes. (I) is useful in gene therapy technique
                                                                                                                                                                                                                                                                                                                                             4189
                                                                                                                                                                                                                                                                                                                                                                                                                              4249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The polypeptide and polynucleotide sequences have applications in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits to assess biodiversity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            a food supplement. (II) and its binding partners are useful in medical imaging of sites expressing (II). (I) and (II) are useful for treating disorders involving aberrant protein expression or biological activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 for identifying expressed genes. (I) is useful in gene therapy techniques to restore normal activity of (II) or to treat disease states involving (II). (II) is useful for generating antibodies against it, detecting or quantitating a polypeptide in tissue, as molecular weight and as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     responsible for biodiversity -
                                                                                                                                                             ABV44141 standard; cDNA; 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5030 BP; 1432 A; 1137 C; 1178 G; 1283 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID
                                                                            16-SEP-2002
                                                                                                                    ABV44141
                                                                                                                                                                                                                                                                                                       361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GAGAGAAGCAACCAACCAACCCAAGGGCAGCAATTTCTGTGTGAAGAACATCAAGC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CACACATCACAGCCCAGACAGACAGGGGGTTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTGACCGCTGTGTGAACATGGATGGGTGGCCAGGCCAACATGATCCTGGATGATGGGG 417
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CACACATCACTGCTCAGACTGCTGTGCTTATGGAAACTCTGGGTGCTCTGGGGGGCCCAGT
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                                                                                                                                                                                                                                                            TCGATAGATGTGTGAATGTGGAGGGCTGGCAGCCAAACATGATCTTGGATGATGGAG
                                                                                                                                                                                                                                                                                                                                                                                     AGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCCGAGTCAGAAGATGACTTCTGGTGGTGTA
                                                                                                                                                                                                                                                                                                                                                                                                                              GCCGATGGGCTGCCTGCAACATCTATTCCACTCTCAATGAAGTGGCTGCTGCTAGCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                            (first entry
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78.7%;
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                                                                                                                                                             BP
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Human; prostate cancer; cytostatic;

carcinogen;

pharmacodyanamic

Human

prostate expression marker cDNA 44132

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RESULT 7
AAZ80766/c
ID AAZ80766 ;
XX
AC AAZ80766;
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Best Local S
Matches 240
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                           patient; (I) is a
                                                                                                                                                                                                                                                                                                                                                                                                                                               in a patient; (e) selecting a composition for inhibiting prostate cancer in a patient; (e) selecting a composition for inhibiting prostate cancer in a compound; (f) assessing the prostate cell carcinogenic potential of a compound; (g) determining whether prostate cancer has metastasized in a patient; (h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-662795/76.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pharmacogenomic
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                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                     322
                                                                                                                                                             382
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                                                                                                                                                                                                                                                                             502
                                                                                                                                                                                                                                                                                                         178
                                                                                                                                                                                                                                                238
                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 240; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          monitoring the progression of prostate cancer in a patient; assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                             GTACACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCCTC
                                                                                                                  GTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGG
                                                                                                                                                                            CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGT
                                                                                                                                                                                                                   AGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG
                                                                                                                                                                                                                                                                                                         GTACACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCCTGGGGGGCTC
                                                                                                   GTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGG
                                                                                                                                                                                                                                                AGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG
                                                                                                                                                                                                                                                                                                                                                                                                                            also
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                                                                                                                                                                                                                                                                                                                                                                                                504
                            standard;
                                                                                                                                                                                                                                                                                                                                                                                                                           useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-183319P.
2000US-189862P.
2000US-207434P.
2000US-211314P.
2000US-211314P.
2000US-255281P.
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 ₽P;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2001WO-US05171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              marker;
                                                                                                                                                                                                                                                                                                                                                                                                 117
                              CDNA;
                                                                                                                                                                                                                                                                                                                                                 57.6%;
                                                                                                                                                                                                                                                                                                                                                                                                A; 150 C; 116 G; 121 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Monahan JE;
                              636
                                                                                                                                                                                                                                                                                                                                     Score 240; DB 23;
; Pred. No. 1e-65;
0; Mismatches 0;
                               ВÞ
                                                                                                                                                                                                                                                                                                                                                                   Length
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   RESULT 8
ABV35309
ID ABV3
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AC ABV3
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-APR-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                        AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The CDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. paracrinomas and sarcomas, e.g. breast or colon cancers. The CDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia, dysplasia or hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-JUN-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 15; Page 469; 469pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acids, used to develop products treatment of disorders involving unwanted cell particularly cancers, especially colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Endege WO,
Carroll E,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-DEC-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hyperplasia;
                               ABV35309 standard;
                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 636 BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-JUN-1998;
                                                                                                     240
                                                                                                                                358
                                                                                                                                                             300
                                                                                                                                                                                          298
                                                                                                                                                                                                                      360
                                                                                                                                                                                                                                                   238
                                                                                                                                                                                                                                                                             420
                                                                                                   GTATTGACCGCTGTGTAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGG
                                                                                                                                                                                                                                                                                            TACACACATCACAGCCCAGACAGC-GGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTC
                                                                                                                                                                             CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGT
                                                                                                                                                              CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGT
                                                                                                                                                                                                                      AGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG
                                                                                                                                                                                                                                                   AGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG
                                                                                                                                                                                                                                                                              TACACACATCACAGCCCAGACAGCGGGGTGTTGATTGAGACACTCTGTGCTCTGGGGGGCTC
                                                                                                                                                                                                                                                                                                                                      ·Conservative
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Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cancer cell line SW480 cDNA clone SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99WO-IB01062
                                                                                                                                                                                                                                                                                                                                                                                                 156 A; 166 C; 137 G; 147 T; 30 other;
                               cDNA;
                                                                                                                                                                                                                                                                                                                                                     54.3%;
99.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KE, Astle JH, Burgess CC,
, Derti A, Ford DM, Lewis
                               312
                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                    Score 226.4; DB 2
Pred. No. 2.3e-61;
                                 ВÞ
                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           proliferation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bushnell SE;
ME, Monahan
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                                                                                                                                                                                                                                                                                                                                        Indels
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                    cancer in a pa
(d) assessing
in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                          The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) sufful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                     Sequence 312 BP; 69 A; 71 C; 102 G; 70 T; 0 other;
                                                                                                                                                                                                                                                                                                                 patient;
(I) is a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 7360-7361; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, uses for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schlegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.
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25-MAY-2000;
                                                                                                                                           238
 233
                            357
                                                        173
                                                                                    298
                                                                                                                113
                                                                                                                                                                      53
                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                          selecting a composition for inhibiting prostate cancer in a patien assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient, assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                   GTACACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTC 237
GGTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGG
              TGTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGG
                                                                    CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATG-ACTTCTGGTGG
                                                                                                                            AGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG 297
                                                                                                                                                                      GTACACACACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGGCTC
                                                      CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGAACTTCTGGTGG
                                                                                                             AGTGTCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG
                                                                                                                                                                                                                                                                                                           also useful as a pharmacodyanamic or pharmacogenomic marker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               æ
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                             the efficacy of a therapy for inhibiting prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression marker cDNA 35300
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                                                                                                                                                                                                                                        54.1%;
98.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Monahan JE;
                                                                                                                                                                                                                           Score 225.8; I
Pred. No. 2.6e
0; Mismatches
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                                                                                                                                                                                                                        2.6e-61;
2;
                                                                                                                                                                                                                                                       DB 23;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                      Length 312;
                                                                                                                                                                                                                                                                                                                                                                                     cancer in a patient;
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RESULT 9
ABV14215
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                                                                                                                                           Query Match
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                             cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(f) assessing the prostate cell carcinogenic potential of a compound;
                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for: (a) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, uses for detecting presence of prostate cancer, stage of prostate cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; prostate pharmacogenomic
                                                                                                                                                                      Sequence 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 2369-2370; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2001-662795/76.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-FEB-2000;
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                                                                              178
                                                                                                                                                                                                    (I) is also useful as a
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                   238
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                                                                                                                         Local
                                                ω
                                                                                                                                                                                                                                determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
AGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG
                                              GTACACACACCAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCCTGGGGGCTC
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                                                                                                            1 Similarity
238; Conserv
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2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                                            Conservative
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                                                                                                                                           useful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                              The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invent
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                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 5561; 21pp + Sequence Listing; English
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P-PSDB; ABB59590.
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                                                                                                                                                                                                                                                                                                                                                 Venter JC,
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                                                                                                                      The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                      (PEKE ) PE
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2000US-0614150.
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                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 40834; 21pp + Sequence Listing; English.
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                                                                                                                                         (PEKE ) PE
                          Claim 1; SEQ ID NO 40831; 21pp + Sequence Listing;
                                                                   New isolated nucleic acid genes from Drosophila and
                                                                                                                                                                                                 23-MAR-2000; 2000US-191637P
11-JUL-2000; 2000US-0614150
 The invention relates to an
                                                                                                              WPI; 2001-656860/75.
                                                                                                                                                                                                                                            23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                          27-SEP-2001
                                                                                                                                                                                                                                                                                                                               Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                        Drosophila; developmental biology; cell signalling; insecticide
                                                                                                                                                                                                                                                                                                    WO200171042-A2
                                                                                                                                                                                                                                                                                                                                                           pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster genomic polynucleotide SEQ ID NO 40831.
                                                                                                                                                                                                                                                                                                                                                                                                                                   26-MAR-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABL29786 standard; DNA; 5537
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66.3%;
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Pred. No. 5.8e-50;
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Best Local Similarity
Matches 275; Conserv
                                                                                                                                                                                                  neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antiinfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative discontinuous; infections discontinuous; cardiovascular; proliferative discontinuous;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
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                                                 08-MAR-2000; 2000WO-US05988
                                                                                                                        WO200055174-A1
                                                                                                                                                                                                                                                                                                                        Human prostate cancer antigen nucleotide sequence SEQ ID NO:439.
                                                                                                                                                                                                                                                                                                                                                                                                                                      AAF16004 standard;
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                                                                                    21-SEP-2000
                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                              13-MAR-2001
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ilarity 66.3%;
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Pred. No. 9.6e-50;
0; Mismatches 140
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            Human; mouse; chicken; rat; secreted expressed sequence tag; SET; expressed sequence tag; EST; probe; chemotactic; proliferative; immunomodulatory; haematopoietic; chemotinetic; analgesic; haemostatic; thrombolytic; antiinflammatory; cytostatic; antibacterial; antifungal; antiviral; antidiabetic; antiasthmatic; vulnerary; antiparkinsonian; antiucer; osteopathic; neuroprotective; nootropic; antipsoriatic; cerebroprotective; anticonvulsant; antidpressant; gene therapy; vaccine; autoimmune disorder; multiple sclerosis; allergic condition; insulin dependent diabetes; asthma; myeloid cell deficiency; ulcer; lymphoid cell deficiency; burn; osteoporosis; osteoarthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostate cancer associated gene sequences, referred to cancer antigens, useful for treatment, prevention, and disorders such as prostate cancer -
                                                                                                                                                                                                          Human segreted expressed sequence tag SEQ ID NO:1381.
                                                                                                                                                                                                                                              21-AUG-2000
                                                                                                                                                                                                                                                                                                              AAA44806 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR15566 to AAR16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to
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(ROSE/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGCTGCTAAAAATAGTGGGCTGTA
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ROSEN C A.
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Pred. No. 5e-46;
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RESULT 15 ABV05046 ID ABV05

ABV05046 standard; cDNA; 328

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298 121 238

CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGCTGGTGCTA 165

CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGCTGGTGCAA

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178 5

GAGAAGCAGCAAACCAACTCCAAGGGCAGCAATTTCTGTGAAGAACATCAAGC

AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT

AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT

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Query Match Best Local S Matches 164

Similarity

39.2%; A; 91 C;

Score 163.4; Pred. No. 1.

.5e-41 DB 21;

Indels

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Gaps

0

237 60 Length

Conservative

0

Sequence

349 BP;

98

87 G;

73 T; 0 other;

exemplification of the present invention.

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nootropic; antiparkinsonian; antipsoriatic; cerebroprotective;
canticonvulsant; and antidepressant. The SESTs can be used for gene
therapy and in vaccines. The SESTs are useful as probes for the
cidentification and isolation of full-length cDNAs and genomic DNA
molecules which correspond to the SESTs. Proteins encoded by the SESTs
are useful in assays for determining biological activity and raising
cantibodies. They may be useful for treatment of autoimmune disorders
(multiple sclerosis, insulin dependent diabetes), allergic conditions
(asthma), myeloid or lymphoid cell deficiencies, wounds, burns, ulcers,
costeoporosis, osteoarthritis, central nervous system disorders
(Alzhelmer's, Parkinson's, Huntington's disease, coagulation
disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's
disease), tumours, bacterial, fungal or viral infections, depression and
psorlasis. AAA45926 to AAA45931 represent linker variants which are given
                                                                                                                                                                                                                                                                                                                                                                                      sequence tags (SESTs), isolated from human, mouse, chicken and rat tissue sources. The SESTs can have a range of activities depending on the tissues they were isolated from. The activities include: chemotactic; proliferative; immunomodulatory; haematopoietic; chemokinetic; analgesic; haemostatic; thrombolytic; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated polynucleotides, and encoded proteins, comprising secreted expressed sequence tags (sESTs), useful for treating various disprders such as autoimmune, infectious, and central nervous system disorders -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Parkinson's disease; Huntington's disease; coagulation disorder; haemophilia; thrombosis; inflammatory disorder; Crohn's disease; tumour; infection; depression; psoriasis; ss.
                                                                                                                                                                                                                                                                                                                                                 cytostatic; antibacterial; antifungal; antiviral; antidiabetic; |
antiasthmatic; vulnerary; antiulcer; osteopathic; neuroprotective;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-317938/27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to AAA45925 represent specifically claimed secreted expressed
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Treacy M,
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Bowman M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Collins-Racie
                                                       fections, depression and variants which are given
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Best Local Similarity
Matches 225; Conserv
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(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                         Sequence 328 BP; 77 A; 67 C; 102 G; 77 T; 5 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 857; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; prostate cancer; cytostatic; carcinogen; pharmacodyanamic marker; pharmacogenomic marker; gene; ss.
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18-JUL-2000;
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                                                                                                                                                                                                                                                          178 GTACACATCACAGCCCAGACA-GCGGTGTTGATTGAGACACTCTGTGCCCTTGGGGGCT 236
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 d) assessing the efficacy of a therapy for inhibiting prostate cancer

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         assessing the aggressiveness or indolence of prostate cancer
                                                                                                                                     CAGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTG 296
                                                                                                                                                                                                             TGGTGGTGTATTGACCGCTGTGTG--AACATGGATGGGTGG--CAGGCCAACATGATCCT 406
                                                         GCTGAGGCTGGAGTTGCAGTGTTCGCTTTGGAAGGGGGCGAGTCANAAGATGACTNCTGGG 198
                                                                            GCTGAGGCTGGAGTTGCAGTGTTCGCTT--GGAAGGGCGAGTCAGAAGATGACTTC----
                                                                                                                                                                                                                                                                                               Conservative
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Db 199 TGGTTGTAATTGGACCGCTGTGTGGAACATTGGATGGGTNGGCAAGGCCAACATGATCCT 258
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Search completed: April 21, 2003, 00:05:25 Job time: 97.5286 secs

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ALIGNMENTS

RESULT 1

	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	HSU82761
Volpe, J.P.G., Busch, D.B., Coleman, D.M., Ziffer, D.W., Yu, Y.,	Cleaver.J.E., Afzal.V., Feenev.L., McDowell.M., Sadinski W.,	1 (bases 1 to 2258) .	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homó.	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	Homo sapiens	Homo sapiens.	·	U82761.1 GI:2852124	U82761	mRNA, complete cds.	ine hydrol	HSU82761 2258 bp mRNA linear PRI 17-DEC-2001	

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                                                                                                                                                                                                                                                                                                                                                                                         232 GAGAGAAGCAACCAACTCCAAGGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGC
                                                                                                                                                                                                                                                                                                                                                         61
                      AGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGGTGTA 360
                                                                                                                                                                         CACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGTGCCCTGGGGGCTCAGT
                                                                                                                                                                                                                                CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA
                                                                                                                                                                                                                                                      CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA 180
                                                                                                                                                                                                                                                                                                                                                                                                               GAGAGAAGCAGCAAACCAACTCCAAGGGCAGCAGCAATTTCTGTGTGTAAGAACATCAAGC 60
                                                                                              CACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGT
                                                                                                                                                                                                                                                                                                              AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT
                                                                                                                                                                                                                                                                                                                                                   AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 120
AGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCCGAGTCAGAAGATGACTTCTGGTGGTGTA
                                                                        GCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (19-DEC-1996) Dermatology, 0750, San Francisco, CA 94143, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trask, B.J., Legerski, R. and Cleaver, J.E. Complementation of chromosomal instability
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Volpe, J.P.G., McDowell, M. and Cleaver, J.E. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nagasawa, H. and Little, J.B.
Increased ultraviolet sensitivity and chromosomal instability related to P53 function in the xeroderma pigmentosum variant Cancer Res. 59 (5), 1102-1108 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Volpe, J.P.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  pigmentosum variant by a gene on human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Inpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .0070969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (bases 1 to 2258)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation-"MATV!TKAPKKQIQFADDMQEFTKFPTKTGRRSLSRSISQSSTDS
YSSAASYTDSSDEVSFREKQOTNSKGSSNFCYKNIKQAEFGRREIEIAEQDMSALIS
LRKRAQGEKPLAGAKIYGCTHITAGTAVLIETICALGACGRWSACNIYSTONEYAAAL
AEAGVAYFAWKGESEDDFWWCIDRCVNNDGWQANMILDDGGDL/THWYYKKYPNYFKI
RGIVEESVTGYHRLYQLSKAGKICYPAMNYNDSYTKQKFDNLYCRESILTWEEVYKINT
VMFGGKQVAVCGYBENGKGCCAALKALGAIVITEIDPICALQACMDGFRVYKLNEVI
RQVDVVITCTGNKNVYTREHLDRMKNSCIVCNNGHSNTEIDVTSLRTEELTWEEVYKLDV
RQVDVVITCTGNKNVYTREHLORMKNSCIVCNNGHSNTEIDVTSLRTEELTWEEVYKLDV
RQVDVVITCTGNKNVYTREHLORMKNSCIVCNNGHSNTEIDVTSLRTEELTWEEVYKDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYLLPKKMDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGPFKPNYYRY"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAC01960.1"
/db_xref="GI:2852125"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'product="S-adenosyl homocysteine hydrolase homolog"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           note="xeroderma pigmentosum variant"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'gene="XPVkona"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell_type="fibroblasts"
tissue_type="skin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McDowell, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 417; DB 9; 1
Pred. No. 3.7e-117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 2258;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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AUTHORS
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KEYWORDS
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JOURNAL
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This clone was selected for full length sequencing because passed the following selection criteria: Hexamer frequency analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (10-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens, S-adenosylhomocysteine MGC:15558 IMAGE:3139729, mRNA, comple BC007576
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       George Yang, Scott Zuyderduyn, Marco Marra
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BC Cancer Agency, Vancouver,
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                               /Product="S-adenosylhomocysteine hydrolase-like 1"
/protein_id="AAH07576.1"
/protein_id="AH07576.1"
/db_xref="GI:14043177"
/db_xref="GI:14043177"
/db_xref="GI:14043177"
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/db_xref="GI:14043177"
/db_xref="GI:1404317"
/
RQVDVVITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLRTPELTWERVRSQ
VDHVIWPDGKRVVLLAEGRLLNLSCSTVPTFVLSITATTQALALIELYNAPEGRYKQD
                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Placenta,
/clone_lib="NIH_MGC_21"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note="Vector:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'clone="MGC:15558 IMAGE:3139729"
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Vancouver, BC, Canada
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complete
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ne hydrolase-like
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Homo sapiens, S-adenosylhomocysteine hydrolase-like
MGC:21453 IMAGE:3450568, mRNA, complete
Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LIML at: http://image.llnl.g Series: IRAK Plate: 20 Row: a Column: 15
This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                             CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
Web site:
http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                            NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 2552)
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2563)
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VMFGGKQVVVCGYGEYGKGCCAALKALGAIVITELDPICALQACMJĞFRVVKLNEVI
RQVDVITCTGNKNVVTREHLDSKNSCIVCMGHSNTE DIVTSLRTPELTWERVRSQ
VDHYIMPDGKRYVLLAEGRILMISGSTYPTFYLSITATTQALALIELYNAPEGRYKQD
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1 637 t
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YSSAASYTDSSDDEVSPREKQOTNSKGSSNFCVKNIKQAEFGRREIEJAEQDMSALIS
LRKRAQGEKPLAGAKIVGCTHITAQTAVLIETLCALGAQCRWSACNIYSTONEVAAAL
AEAGYAVFANKGESEDDFWWCIDRCVNNDGWQANMILDDGGDLTHWVYKKYPNVFKKI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Placenta, choriocarcinoma"
/clone_lib="NIH_MGC_10"
/lab_host="DH10B"
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/db_xref="GI:16877387
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/db_xref="taxon:9606"
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Pred. No. 3.7e-117;
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                                                                                                                                                                                       TTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGG
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Patent: W
                                                                      Homo sapiens, S-adenosylhomocysteine hy MGC:8936 IMAGE:3853747, mRNA, complete BC010681
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//db_xref="GI:10190061"
//db_xref="GI:10190061"
//tans1afid1on="RGQVGARSCCFWFSCGHRRCPAALGCRTDKAWATAPQKPTQLDA
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AGGRRVGDRVSEGAARAGGRAPEGERGGGGSAAGRAGGGMSHDAMPLEGVGSEDLSYS
GAASYTDSSDDEVSPREKQQTNSKGSSNECVKNIKQAEFGRREIEIAEQDMSALISLR
KRAQGEKPLAGAKIVGCTHITAQTAVLIETLCALGAQCKWSACNIYSTQNEVAAALAE
-AGYAVFAWKCESEDDFWWCLDRCVNNDGWQANNILDDGGDLTHWYYKKYPNVFKKIRG
IVEESVTGVHRLYQLSKAGKLCVPAMNVDSVTKQKFDNLYCCRESILDGLKRTTDVM
FGGKQVVVCGYGEVGKGCCAALKALGAIVYITEIDPICALQACXBGFRVVKLNEYIRQ
VDVVITCTGUKNNVTREHLDBMKNSCIVCNNGHSNTELDVTSLRTPELTWERVRSQVD
HVIWPDGKRVVLAEGRLLNLSCSTVPTFVLSITATTQAALIELYNAPEGRYKQDVY
LLPKKNDEVYASLHLPSSFDAHLTELTDDQAKYLGLNKNGPFKPNYYRY"
46 a 604 c 677 g 636 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the full 5' nucleotide yet to be identified."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Open reading frame extends without a stop codon the full 5' nucleotide sequence. The initiation codon l
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/db_xref="taxon:9606"
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Pred. No. 3.7e-117;
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CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA
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CACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCCTGGGGGCTCAGT
                                             CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA
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This clone was selected for full length sequencing passed the following selection criteria: matched mR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: villaion@bcm.tmc.edu.
Villaion, D.K., Luna, R.A., Hale, S.M., Hul
A.M., Holloway, M., Telford, B, Hodgson, A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
COntact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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LRKRAGEKPLAGAKIVGCTHITAQTAVLIETLCALGAQCRWSACNIYSTQNEVAAAL
AEAGYAVFAMKGESEDDFWGC. IDRCVNNDGWQANMILDDGGDLHWVYKKY PAVFKKI
RGIVEESVTGVHRLYQLSKAGKLCYPAMNVNDSVTKQKFDNLYCCRESILDGLKRTTD
VMFGCKQVVVCGYGEVGKGCCAALKALGAIVY ITEIDPICALQACMDGFRVVKLNEVI
RQVDVVITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLRIPELTWERVRSQ
VDHVIWPDGKRVVLLAEGRILNLSCSTVPTFVLSITATTQALALIELYNAPEGRYKQD
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/product="S-adenosylhomocysteine hydrolase-like
/protein_id="AAH10681.1"
/db_xref="GI:14715038"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="Colon, adenocarcinoma"
/clone_lib="NIH_MGC_65"
/lab_host="DH10B"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               translation="MATVTKAPKKQIQFADDMQEFTKFPTKTGRRSLSRSISQSSTDS"
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Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (23-OCT-2000) Dendritic Cell Research, Mater Medical Research Institute, Level 3, Aubigny Place, South Brisbane,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Dekker, J.W., Budhia, S. Hart, D.N.J. and Kato, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Identification of an S-adenosylhomocysteine hydrolase-like transcript induced during dendritic cell differentiation Immunogenetics 53 (12), 993-1001 (2002)
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Dekker, J.W., Budhla, S., Angel, N.Z.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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LIETLCALGAQCRWSACNIYSTQNEVAAALAEAGVAVFAWKGESEDDFWWCIDRCVNM
DGWQANNILDDGGDLHWYKKYPNYFKKIRGIVEESYTGVHLYQLSKAGKLCVPAM
NVNDSVTKQKFDNLYCCRESILDGLKRTTDVMFGGKQVYVCHFLYQLSKAGCCAALKALG
AIVYITEIDPICALQACMOGFERVKLMEVIRQVDVVITCTGNKNVYTREHLDRAKKSC
IVCNMGHSNTELDVTSLRTPELIWERVRSQVDHVIWPDGKRVVLLAEGRLLNLSCSTV
PTFYLSITATTQALALIELYNAPEGRYKQDVYLLPKKMDEYVASLHLPSFDAHLTELT
                                                                                                                                                                                                                                    /note-"DCAL; dendritic cell expressed AHCY-like protein; expressed in dendritic cells in blood, Langerhans cells and dermal dendritic cells; mRNA increased during monocyte differentiation to monocyte-derived dendritic cells in the presence of GM-CSF and IL-4"
                                                                                                                                     /translation-"MSMPDAMPLPGVGEELKQAKEIEDAEKYSFMATVTKAPKKQIQF
ADDMQEFTKFPTKIGRRSLSRSISQSSTDSYSSAASYTDSSDDEVSPREKQQTNSKGS
                                                                                                                                                                /product="S-adenosylhomocysteine hydrolase-like protein"
/protein_id="AAL26869.1"
/db_xref="GI:16588687"
                                                                                                                                                                                                                                                                                                                                                                           /cell
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/db_xref="taxon:9606"
/chromosome="1"
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                                                                                                                                                                                                                                                                                                                                             'note-"derived from 5'
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                                                                                                                                                                                                                                             please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14% Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Fuither information about the clone and the sequencing project is aviat http://www.mips.biochem.mpg.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                    Martinsried, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German
Clone from S. Wiemann, Molecular Genome Analysis, German
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.c
sequenced by AGOWA (Berlin/Germany) within the cDNA seque
consortium of the German Genome Project.
This clone (DKFZp564A1523) is available at the RZPD in Be
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (15-MAY-1999) MIPS, Martinsried, GERMANY
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(bases 1 to 2510)
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                                        /clone_lib="564 (synonym: hfbr2). Vector pAMP1 X1-2blue; sites NotI + SalI"
                                                                                                          /db_xref="taxon:9606"
/map="1, 15.55 cR from D1S248"
/clone="DKFZp564A1523"
                                                                                                                                                                                                         1. .2510
/dev_stage="fetal"
1. .1796
                                                                                   /tissue_type-"brain"
                                                                                                                                                            /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                             al Similarity
416; Conserv
                                                                                                                             mus musculus, S-adenosylhomocysteine hyc
MGC:18748 IMAGE:4007102, mRNA, complete
BC018218 GI:17390492
MGC.
   Submitted
                                Strausberg, R
                                             Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; 1 (bases 1 to 1772)
                                                                                                  Mus musculus
                                                                                                               house mouse
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Submission 
Led (03-DEC-2001) National Institutes
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KQOTNOKGSSNFCVKNI KQAEEGRRE IE IAEQDMSALI SLRKEAQGKKPLAGAK I VGC
THITAQTAY VLIETLCALGAQCENSACHI Y STQNEVAAALAEAQVA VFAMKGESSDDEVK
WCIDRCVNMDGGAQANMILDDGGDLTHMYYKKY ENVEKKI RGI VEESYTGYHRLY QLSK
AGKLCVFAMNVNDSVTKQKFDNLYCCRES ILDGLKRTTDVMFGGKQVVVCGYGEVGKG
CCAALKALGAIVI ITELDPI CALQACMGFRVVKLNEV I RQVDVYITCTGNKRVVTRE
HLDRMKNSCI VCNMGHSNTEIDVTSLRT PELTWERVRSQVDHVIWPDGKRVVLLAEGR
LLNLSCSTVPTTVLS ITATTQALALI ELYNAPBGRYKQDVYLLPKKNDEYVASLHLPS
EDAHLTELTDDQAKYLGLNKNGPFKPNYYRY
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<1. .1796
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TQAPSGESENLRNLRQGRRAESSQNLLSLRRLVSAQGNGRSDWRWLWIQLWPEIDSLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
/protein_id="CAB43223.1"
/db_xref="GI:4884204"
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splice variant"
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Pred. No. 1.2e
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1 GAGAGAAGCAACCAACTCCAAGGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGC
CACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCCTGGGGGCTCAGT
                                                                                CACTCAGGAAACGTGCTCAGGGAGAGAAGCCTTTGGCTGGTGCTAAAATAGTGGGCTGTA
                                                                                                                                                                                                                                                                                                                                                                                                              GAGAGAAGCAGCAAACCAACTCGAAGGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGÇ
                                                                                                                  CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA
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Email: cyapbs-remail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone distribution: MGC clone distribution information can through the I.M.A.G.E. Consortium/LLNL at: http://image.lln Series: IRAK Plate: 23 Row: n Column: 6 Plate: 23 Row: n Column: 6 Plate: 25 Row: n Column: 6 Plate: 10 Plate: 25 Row: n Column: 6 Plate: 10 Plate: 27 Row: n Column: 6 Plate: 10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, (
Yoon, V.S., Kowis, C.R., Lawrence, S., Martin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gene Colle
Institute,
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Contact: MGC help des
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VDHVTMPDGKRVVLLABGRLLMLSCSTVPTFVLSITATTQALALIELYNAPEGRYKQD
VYLLFKKMDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGPFKPNYYRY
1 406.c 506 g 398 t
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/translation="MATVTKARKKQIOFADDMOEFTKFFTKTGRRSLSRSISGSSTDS
/translation="MATVTKARKKQIOFADDMOEFTKFFTKTGRRSLSRSISGSSTDS
YSSAASYTDSSDDEVSFREKQOTNSKGSSNFCVKNIKQAEFGRREIEIAEQDMSALIS
LRKRAGGEKPLAGAKIVGCTHITAQTAVLIETLCALGAQCRMSACNIYSTQNEVAAAL
AEAGYAVFAMKGESEDDFWMCIDCVKNDGWQANMILDDGGDLTHWVYKKYPWFKKI
RGIYEESYTCYHTLYOLKAKGKLVPAMNYNDSVTKOKEDNLYCCRESILDGLKRTKU
VMFGGKQVVVCGYGEVGKGCCAALKALGAIVYITEIDPICALQACMDGFRVVKLNEVI
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MMTV-LTR/Wntl model. Expression driven by an MMTV-LTR
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/protein_id="AAH18218.1"
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/clone="MGC:18748 IMAGE:4007102"
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/lab_host="DH10B"
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/db_xref="taxon:10090"
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Pred. No. 2.6e-107;
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JOURNAL REFERENCE
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AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (29-AUG-2000) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure Analysis, Human Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan (E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286, Fax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-& 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara,T., Nakamura,Y., Isogai,T. and Sugano,S.
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Homo sapiens colon mucosa cDNA to mRNA, clone_lib:ColF
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Homo sapiens cDNA: FLJ21719
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gano,S., Suzuki,Y., Ota,T., Obayashi,M., Nishi;T., Isogai,T.,
ibahara,T., Tanaka,T. and Nakamura,Y.
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Direct Submission
Submitted (25-MAY-2001) National Institutes of Health, Mammalian Submitted (25-MAY-2001) National Institutes of Health, Mammalian Sene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Institutes of Health, Mammalian Submission (MGC), Cancer Genomics Office, National Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Canc
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CDNA Library Arrayed by: The I.M.A.G.E. CO
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lnfo@bcgsc.bc.ca
                                                                                                                                                                                                                                                                                                                                                          the I.M.A.G.E. Consortium/LLNL
IRAL Plate: 23 Row: j Column: 1
              /codon_start=3
/product="Similar to S-adenosylhomocysteine hydrolase-like
1"
                                                                                                                                     /tissue_type="Lung, small
/clone_lib="NIH_MGC_7"
/lab_host="DH10B-R"
                                                                                                                                                                                                                    /clone="IMAGE: 3536052"
                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                           note="Vector:
                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                     .1838
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                                                                                                                                                                                                                                                                                                                                                                                   information can be found http://image.llnl.gov
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) Jeff Stott,

Jill Vardy,
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BASE COUNT ORIGIN

Matches

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Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GCCGCTGGTCTGCTAACATCTACTCAACTCAAATGAAGTAGCTGCAGCACCTGGCTG
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                                                                                       Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O. Prediction of the coding sequences of unidentified human genes. XII. The complete sequences of 100 new cDNA clones from brain w code for large proteins in vitro
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens mRNA for KIAA0828 pAB020635
2 (bases 1 to 5025)
Ohara, O., Suyama, M., Kikuno, R., Nagase, T. and Ishikawa, K.
Direct Submission
Submitted (02-DEC-1998) Osamu Ohara, Kazusa DNA Research
                                                                                                                                                    1 (sites)
Nagase,T., Ishikawa,K., Suyama,M.,
Miyajima,N., Tanaka,A., Kotani,H.,
                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                              Homo sapiens adult male brain cDNA SK plus clone:hh04230
                                                                                                                                                                                                                                                                                                                                           AB020635.1
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Similarity 78.78;
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EALVSPDGTVTEAPRTVKKQIOPADQRGENKRETKIGRRSLSRISQSSTDSYSSAA
SYTDSSDDETSFRDKQQKNSKGSSDFCYKNIKQAEFGREIEIAEQEWALMALKAR
GEKPLAGAK I VGCTHITAQTAYLMETLGALGAQCRWAACNI YSTLNEWAALAESGF
PYAWKGESEDDFWWCIDRCVNVEGWQPMILDDGGDLTHWIKXYPANFKKIKGIVE
ESVTGVHRLYQLSKAGKLCVPAMNVNDSVTKQKEDNLYCCRESILDGLKRTTDMFGG
KQVVCCYGEVCKGCCAALKAMGSIVYYTEIDFICALQACMDGFRLYKLNEVIRQVDI
VITCTGNKNVYTREHLDRMKNGCIVCNMGHSNTEIDVASLRTPELTWERVRSQVDHVI
WPDGKRIVLLAEGRLLUNGSSTVPTFVLSITATTQALALIELYMAPEGRYKQDVYLLP
WPDGKRIVLLAEGRLLUNGSTYPTFVLSITATTQALALIELYMAPEGRYKQDVYLLP
KKMDEYVASLHLPTDAHLTELTDBGAKYLGLNKNGFFKPNYRR
492 C 548 g 451 t
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/db_xref="GI:14249936"
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Pred. No. 2.5
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                                                                                                                                                                                                                                                                                                                                                                            protein,
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 Kazusa DNA Research Institute,
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Matches 328
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241

700 181 640

580

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JOURNAL MEDLINE REFERENCE AUTHORS

JOURNAL

REFERENCE AUTHORS

TITLE

ACCESSION VERSION

DEFINITION SD307

SOURCE KEYWORDS

ORGANISM

RESULT 11 AB020635

밁 Ş 밁 Ş 밁

980

361

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TCGATAGATGTGTGAATGTGGAGGGCTGGCAGCCAAACATGATCTTGGATGATGATGAG
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BC024325
Homo sapiens, KIAA0828
mRNA, complete cds.
BC024325
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KKIKGIYESVYGOVHRLYQLSKAGKLCYBAMVVDSVYRKQKFDNLYCCRESILDGLKR
TIDMMFGGKQVVVCGYGEVGKGCCAALKAMGSIYYVTELDPICALQAGMGFRLVKLN
EVIRQVDIVITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVASLRTPELTWERV
EVIRQVDIVITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVASLRTPELTWERV
ESQVDHYIWPDGKRIVLLAEGRLLNLSCSTVPTTVLSITATTQALALIELYNAEBGRY
KQDVYLLPKKMDEYVASLHLPFTDALALIELTDEQAKYLGLNKNGPFKPNYYRY*
A 1179 C 1136 g 1429 t
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TDSYSSAASYTDSSDDETSPRDKQQKNSKGSSDFCVKNIKQAEFGRREIEIAEQEMPA
LMALKRAQGEKPLAGAKIVGCTHITAQTAVLMETLGALGAQCRWAACNIYSTLNEVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="Epvvaaeavmsvqvvsaaaaakvpevelkdlspseaesqlglst
aavgamappagggdpeapapapaaerppvpgpgsgpaaalspaagkvpqasamkrsdphh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="BAA74851.1"
/db_xref="GI:4240145"
/translation="""""
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/clone_lib="pBluescriptII SK plus"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="KIAA0828"
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/db_xref="taxon:9606"
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78.7%;
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Pred. No. 2.5e-73;
0; Mismatches 89;
                                             5052 bp
protein,
                                             clone MC
                                             NA linear PRI 12-MAR-2002
MGC:21525 IMAGE:3907552,
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.jp, Tel:+81-438-52-3913
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  AGGCAGAGTTTGGACGAAGAAATTGAAATTGCTGAACAAGAAATGCCTGCATTGATGG 691
                                   AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 120
                                                                            GGGACAAGCAGCAAAAGAACTCTAAGGGAAGCAGTGACTTCTGTGTTAAGAACATCAAAC 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/ILML at: http://image.linl.geries: IRAK Plate: 22 Row: 1 Column: 29 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
Submitted (01-MAR-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo
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MGC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Institute, 31 Center Drive, Room
                                                                                                                                                                           Similarity
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SYTDSSDDETSPRDKQQKNSKGSSDFCVKNIKQAEFGRREIEIAEQEMPALMALRKRA
QGEKPLAGAKIVGCTHITAQTAVLMETLGALGAQCRWAACNIYSTLNEVAAALAESGF
                                                                                                                                                                                                                                                                           WPDGKRIVLLAEGRLLNLSCSTVPTFVLSITATTQALALIELYNAPEGRYKQDVYLLP
KKMDEYVASLHLPTFDAHLTELTDEQAKYLGLNKNGPFKPNYYRY"
                                                                                                                                                                                                                                                                                                                                       PVFAMKGESEDDFWWCIDRCVNVEGWQPNMILDDGGDLTHWIYKKYPNMFKKIKGIVE
ESVTGVHRLYQLSKAGKLCVPAMNVNDSVTKQKFDNLYCCRESILDGLKRTTDMMFGG
KQVVVCGYGEVGKGCCAALKAMGSIVYVTEIDPICALQACMDGFRLVKLNEVIRQVDI
                                                                                                                                                                                                                                                                                                                    VITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVASLRTPELTWERVRSQVDHVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="KIAA0828 protein"
/protein_id="AAH24325.1"
/db_xref="GI:19353092"
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/db_xref="LocusID:23382"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                             agggdpeapapaaerppypgpgsgpaaalspaagkypqasamkrsdphhqhqrhrdgg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_11b="NIH_MGC_71"
/lab_host="nuin="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone="MGC:21525 IMAGE:3907552"
/t1ssue_type="Uterus, leiomyosar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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78.7%;
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                                                                                                                                                                                                                                                        1145 g
                                                                                                                                                                           Score 274.6;
Pred. No. 2.5
                                                                                                                                                         Mismatches
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                                                                                                                                                 sequence clones from Drosophila Gene Collection 1 (Rubin et al., science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polyA tail and contiguity within 100 kb in the genome. Thus we believe the sequence to reflect accurately this particular cDNA clone. However, there are artifacts associated with the generation of cDNA clones that may have not been detected in our initial analyses such as internal priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs) and reverse transcription of unspliced precursor RNAs and reverse transcription about this sequence, including its location and relationship to other sequences, please visit our Web site (http://fruitfly.berkeley.edu) or send email to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCGATAGATGTGTGAATGTGGAGGGCTGGCAGCCAAACATGATCTTGGATGATGGAG
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(bases 1 to 1792)
Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J. Champe, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Fri George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Lia Miranda, A., Mungall, C.J., Nunoo, J., Pacleb, J., Paragas, V., Patel, S., Phouanenavong, S., Wan, K., Yu, C., Lewis, S.E., Rubin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (16-MAY-2002) Berkeley Drosophila Genome Project, Lawrence Berkeley National Laboratory, One Cyclotron Road,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Lawrence Berkeley National Laboratory
/strain="y; cn bw sp"
/db_xref="taxon:7227"
/map="89E10-89E10"
                                                                                    organism="Drosophila"
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., Park,S.
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/map-

/gene="Ahcy89E"

/note="alignment with genomic scaffold AE003715"
/db_xref="FLYBASE:FBgn0015011"

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RESULT 14
AC020395/c
LOCUS
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AUTHORS
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Rockville, MD, USA
Rockville, MD, USA
This sequence was identified as CDM:10213028 by the submitter
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This sequence was identified as CDM:10213028 by the submitter
                                                                                                                  Drosophila melanogaster.
Drosophila melanogaster
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Drosophila melanogaster
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 52423)
                                                        Direct Submission
Submitted (30-DEC-1999) Celera Genomics,
                                                                                                                                                                                                                                                                                              Drosophila melanogaster,
                                                                                              Adams, M. and Venter, J.C.
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DGRMIILLAEGRLVNLSCSTISSFVVSVASSTQALALIELFSAPGRYKSDVYLLPKKM
DEYVASLHLATFDAHLTELTDEQSKFMGLNKAGPFKANYYRY"
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VTGVHRLYMLSKGGKLTVPAINVNDSVTKNKFDTFYTCRDSILDSLKRTTDIMFGGKQ
VVICGYGDVGKGCAQSLKGQGCIVYVTEVDPICALQAAMDGFRVVRLNEVIRTVDVVV
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GSSDEEDVSFKDNHQRNSAGGTDFCVKSISKSAFGRREIEIAESEMPGIMTLRKRAKD
EKPLKGANIVSCTHYVAQSAVLIETLYQLGATYRWAACNIYSTQNAVAAALAEAGIPI
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/note="Longest ORF"
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                                                                                                                                                DeLorenzi,M., Ali,N., Saari,G., Henry,C., Wilcox,M. and Bienz,M. Evidence that the Abdominal-B r element function is conferred by
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Cell 43 (1), 71-80 (1985)
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                                                                                                EMBO J. 7 (10), 3223-3231 (19)
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Ephydroidea; Drosophilidae; Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster (tissue library: P1) adult whole Drosophila melanogaster
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Zavortink,M. and Sakonju,S
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This sequence will be replaced
by the finished sequence as soon as it is
the accession number will be preserved.
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Pred. No. 1.4e-47;
0; Mismatches 140
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                                                                                                                             363 GACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGG 417
                                                                                                                                                                                                                                                  303 GCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATT 362
                                                                                                                                                                                                                                                                                                                              243 CGCTGGTCTGCTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAG 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3 GAGAAGCAGCAAACCAACTCCAAGGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGCAG 62
                                                                                                                                                                                                GCGGGAATTCCGATCTTCGCCTGGCGCGGAGAGACCGGAGGAGGAGGAGTTCTGGTGGTGCTTG 3701
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Martin, C.H., Celniker, S.E., Davis, C.A., Mayeda, C.A.,
Strathmann, M.P., Yoshida, K. and Palazzolo, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nes Dev. 3 (12A), 1969-1981 (1989)
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16747 c 16641 g 23596 t
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b_xref="taxon:7227"
ap="3,89E; polytene"
issue_type="whole fly"
ev_stage="adult"
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Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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417
1 gagagaagcagcaaaccaac
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Match
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1: /cgn2_6/ptodata/1
2: /cgn2_6/ptodata/1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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4483
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US-08-204-740-8

US-09-081-395-8

US-09-081-395-8

US-09-416-33-8

PCT-US95-02521-8

US-09-081-395-6

US-09-081-395-6

US-09-081-395-6

US-09-416-33-6

PCT-US95-02521-6

US-08-632-463B-1

US-08-658-136-2

US-08-658-136-2

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US-08-658-136-1

US-08-658-136-1

US-08-658-136-1

US-08-658-136-2

US-09-114-078-2

US-09-134-078-2

US-09-488-8568-10

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1, Appl	Sequence	US-08-650-598-1	Ŋ	1611	6.7	27.8	٠.
1, Appl	Sequence	US-09-761-716-1	4	1875	6.7	28	_
9, Appl	Sequence	US-09-103-489-9	4	500	6.7		_
9, Appl	Sequence	US-08-627-706-9	Ь	500	6.7	28	
5, Appl	Sequence	US-09-103-489-5	4	308	6.7	28	-
5, Appl:	Sequence	US-08-627-706-5	Ь	308	6.7	28	Ŭ
60, App	Sequence	US-08-961-527-60	4	6827	6.8	28.2	•
10, App.	Sequence	US-09-085-199B-10	4	3979	6.8	28.2	_
1, Appl:	Sequence	US-08-916-352-1	4	3879	6.8	28.2	_
4, Appl:	Sequence	US-09-220-641-4	4	5816	6.9	28.6	٠.
263, App	Sequence	US-08-961-527-263	4	3744	.6.9	28.6	٠.
113, Ap	Sequence	US-08-961-527-113	4	18627	6.9	28.8	_
1, Appl:	Sequence	PCT-US94-01782-1	ű	2384	7.0	29	_
1, Appl:	Sequence	US-08-726-160-1	۳	2384	7.0	29	
1, Appl:	Sequence	US-08-021-608D-1	_	2384	7.0	29	•
9, Appl:	Sequence	PCT-US94-01782-9	ر.	2381	7.0		_
9, Appl:	Sequence	US-08-726-160-9	μ	2381	7.0	29	_
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ALIGNMENTS

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298	360	238	420	. 179	Matches	Query Match	09-328	OTHER INF	NAME/I	FEATURE:	ORGANISM:	LENGTH:	SEO ID NO	NUMBER	EARLIER	EARLIER	CURRENT	FILE R	TITLE OF		APPLICANT	APPLICANT	DESTINATION	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT	APPLICANT:	Г,	Sequence Patent No	RESULT 1 US-09-328-	
CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGT	AGTGCCGCTGGTCTGCTAAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG	AGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG	TACACACATCACAGCCCAGACAGCGGGTGTTGATTGAGACACTCTGTGCTCTGGGGGCTC	TACACACATCA	8; B;	tch	09-328-111-850	INFORMATION: n			HOMO	636	850	SEQ ID N	FILING DATE:	APPLICATION	15	ERENCE:	T INVENTION:	i	: Monahan	: Lewis,	י בסדת ז	: Catino,	••	••	•• •	• ••	••	INFORMATION:	0. 626 626	111-8	
STTGCAGTGTT	CTGCTTGTAA	CTCCTTGTAA	CAGCCCAGACA	CAGCCCAGACA	Va.	54.38;		n = A,T,C	ture		ganteng .		TOT WINDOWS			NUMBER: US	NUMBER: U		: NOVEL HUMAN GENES	•	, John E.	Marcia E.	ACHAH M	Theodore J	III, Eddie	Bushnell, Steven E.	Burgess, Christopher	nn, Kathleen	Wil	••	Application US/0 52333		
CGCTTGGAAG	CATCTACTCA	CATCTACTCA	GCGGGTGTTG	GC-GGTGTTG	Pred. No. 4e- 0; Mismatches	Score		or G					version	Word on		S 60/088,801	NUMBER: US/09/328,111							•			er C.	Ď.			08/09328111		
GGCGAGTCA	ACTCAGAAT	ACTCAGAAT	ATTGAGACA	ATTGAGACA	tches		•			•			0.0			01	11		AND GENE E														
GAAGATGAC	GAAGTAGCT	GAAGTAGCT	CTCTGTGCT	CTCTGTGCC	1; Indels	4; Length		•											EXPRESSION														
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300 CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGT

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US-09-347-878 2
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                                                                                  GENERAL INFORMATION:
APPLICANT: YUAN, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 25885-1651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 224;
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Best Local Similarity
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LENGTH: 2211
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
CURRENT APPLICATION NUMBER: US/09/347,878C CURRENT FILING DATE: 1999-07-06 NUMBER OF SEQ ID NOS: 75 SOFTWARE: Patentin Ver. 2.0 SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -09-318-448-26
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CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
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APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING,
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 601-1-057
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PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: M61831/GenBank
US-09-347-878-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1,
Patent No. !
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Best Local Similarity
Matches 224; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
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FILING LALL:
CLASSIFICATION: 80U
ATTORNEY/AGENT INFORMATION:
NAME: MURPHY JR, GERALD M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: BIRCH, STEWART,
STREET: PO BOX 747
                                                                                                      SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  139 GCCTGATGCGTATGCGGGAGCGGTACTCGGCCTCCAAGCCACTGAAGGGCGCCCGCATCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 112 CTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAG 171
                                                                                                                                                                                                                                      STREET: FO LUNCH
                                                                                                                      SOFTWARE:
                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                         COUNTRY: USA
ZIP: 22040-0747
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   79 ACATCGGCCTGGCTGCCTGGGACGCCAAGGCCCTGGACATTGCTGAGAACGAGATGCCGG 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ACGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Application US/08669536
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                                                                                                                                                                                                                                                                                                                                                                              KUWATA,
                                                                                                                                                                                                                                                                                                                                                                                            TANAKA,
                                                                                                                                                                                                                                                                                                                                                                                                               UEHARA,
                                                                                                                                                                                                                                                                                                                                                                                                                             MASUTA,
                                                                                                                                                                                                                                                                                                                                         SHIGERU
ORGANISMS IN WHICH THE EXPRESSION OF
S-ADENOSYLHOMOCYSTEINE HYDROLASE GENE
                                                                                                                                                                                                                                                                                                                                                                                                                             CHIKARA
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61.2%;
                                                                                                                                                                                                                                                                                                                                                                                            HIDEO
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                                                                                        US/08/669,536
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Pred. No. 5.7e-36;
                                                                                                                                                                                                                                                                                          KOLASCH
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                                                                                                                         Version #1.30
                                                                                                                                                                                                                                                                                          AND
                                                                                                                                                                                                                                                                                          BIRCH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-08-930-894-
                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08930894 Patent No. 6037524
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 57. Matches 232; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: GREENL
APPLICANT: DRAPER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (703) 205-8050 INFORMATION FOR SEQ ID NO: 1:
        OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: MS WORD
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/930,894
FILING DATE: 09-OCT-1997
                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: cDNA to mRNA
                                                                                                                                                                                                                                                                                                           TUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           262 ACTGCAGTTTTGAATAACCCTTACTGCTTTGGGTGCTGAAGTTAGATGGTGTTCTTGC 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      142 CTTGAAATCGAGCTGGCCGAAGTTGAAATGCCTGGTCTCATGGCTTGTCGTACTGAATTT
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                           CITY: Washington
STATE: 的 D.C.
                                                                                                                                                                                                                                                                                                                               TLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            78
                                                                                                                                                                        COUNTRY: U.S.A. ZIP: 20005-3918
                                                                                                                                                                                                                                                STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 AAGACCACCTCTGGCCGCGAGTACAAGGTCAAGGACATGTCTCAGGCCGATTTCGGCCGG 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
CLASSIFICATION:
                                                                                                                                  MEDIUM TYPE:
                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTGATTGACCGCTGTGTGAAC: 377
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                                                                                                                                                                                                                                                  E: Pillsbury Madison & Sutro
1100 New York Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                    DRAPER, John
SKIPSEY, Marc
                                                                                                                                                                                                                                                                                                                                             WARNER, Simon
                                                                                                                                                                                                                                                                                                                                                                                                          GREENLAND,
                                                                                         E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                               S-ADENOSYL-L-HOMOCYSTEIN HYDROLASE PROMOTER
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                                                                                                                                                                                                                                                                                                                                                                                                        Andrew James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1254-128
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Pred. No. 3.2e-29;
0; Mismatches 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          417
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 190;
                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORIGINAL SOURCE: ORIGIN
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LENGTH: 1767 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 10-APR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                             CORRESPONDENCE ADDRESS
                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                TITLE OF INVENTION:
                                                                                                                                                                                                               TITLE OF INVENTION: Methods for Identifying
                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 TTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGGAGAAGC 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31 GCAGCAATTTCTGTGTGAAGAACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGAGA 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LODOTOGA:
                                     DDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCG 367
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E: Allgretti & Witcoff, Ltd.
10 S. Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                      Mazo, Ilya
                                                                                                                                                                                                                                             Roninson,
                                                                                                                                                                                                                                                                                                                               Kazarov, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                         Growth in Cancer Cells
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Pred. No. 8.1e-24;
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                                                                                                                                                                                  Genes Associated with Malignant
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COMPUTER READABLE FORM:

COUNTRY: U

Chicago

Illinois

COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS

Floppy disk

PatentIn Release #1.0, Version #1.25

MEDIUM TYPE: COMPUTER: II

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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
                                                                                                                                                                                                                                                                                   APPLICANT: RONINSON, TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 312-715-1000
TELEPHONE: 312-715-1234
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NAME: No. 5753432nan, Kevin
REGISTRATION NUMBER: 35,303
               SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:
                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 04-MAI
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 APPLICATION NUMBER:
                                                                                                                                                COUNTRY:
                                                                                                                                60606
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                                                                                                                                                                      Illinois
                                                                                                                                                                                                   E: McDonnell Boehnen Hulbert & Berghoff
300 S. Wacker Drive, 32nd Floor
                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                        Roninson,
                                                                                                                                                                                                                                                                                                                                                                                Kazarov, Alexander
                                                                                                                                                                                                                                                                                                                                                                Mazo,
                                                                                                                                                                                                                                                                                                                                                                                                   Gudkov, Andrei
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                                                                                                                                                                                                                                                                                   Suppressor Elements and Growth in Cancer Cells
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Suppressor Elements and Genes Associated with Malignant
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US/09/081,167A
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Pred. No. 1.4e-14;
0; Mismatches 89;
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Patent No. 6083746
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Best Local Similarity 58.6%;
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NAME: NO. 6083745nan, Kevin
REGISTRATION NUMBER: 35,303
          SOFTWARE: Patentin Release #10, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/081,395
FILING DATE: 18-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6083746nan, Kevin E
REGISTRATION NUMBER: 35,303
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                        STREET: 500
CITY: Chicago
CTTE: Illinois
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
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                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: TITLE OF INVENTION:
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TOPOLOGY: 11r
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                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 289 base pairs TYPE: nucleic acid
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                             300 S. Wacker Drive,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gudkov, Andrei
                                                                                                                                                                                                                                                                                                                                                                                                                     Roninson,
                                                                                                                                                                                                                                                                                               McDonnell Boehnen Hulbert & Berghoff
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                                                                                                                                                                                                                                                                                                                                                                Suppressor Elements and Growth in Cancer Cells
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93,354-KK
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                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                       ATTORNEY/AGENT INFORMATION:
NAME: NO. 619752Lnan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93
                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000
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                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
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                                                                                                                                                                                     COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                    CLASSIFICATION:
                                                                                           APPLICATION NUMBER:
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10 S. Wacker Drive, Suite 3000
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Methods for Identifying Genetic
Suppressor Elements and Genes Associated with Malignant
Growth in Cancer Cells
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58.6%;
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US-09-416-833-8
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GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
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 CTGGCTGCCTGCACATGACCGTGGAGACGGCCGTCCTCATTGAGACCCT
                               CTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGCTGGTGCTAAAATAG
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Suppressor Elements and
Growth in Cancer Cells
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Pred. No. 1.
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Pred. No. 1.4e-14;
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Genes Associated with Malignant
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tent No. 575343
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
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CITY: Chicago
STATE: Illinois
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: NO. 5753432nan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93
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MEDIUM TYPE: Floppy
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                                                                                                                                   124 ATGGEAGGGTTGATGCGCATGCGGGAGATGTACTCAGCCTCCAAGCCACTGAAGGGTGCT
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                                                                    184 CGCATTGCTGGCTGCCTGCGCATGACCGTGGAGACTGCTGTTCTCATTGAGACTCTCGTG 243
                                                                                                      64 GTCGCGGACATCGGACTGGCCGCCTGGGGACGGAAGGCTCTGGATATAGCTGAGAATGAG 123
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                               GCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTAC 266
GCCCTGGGTGCTGAGGCGCGCGGTGCTCCAGCTGCAACATCTTC 285
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DEDNESS: single
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10 S. Wacker Drive, Suite 3000
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Suppressor Elements and Genes Associated with Malignant
Growth in Cancer Cells
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                                                                                                                                                                                                                                                                                      Score 68.4; DB 1;
Pred. No. 3.4e-13;
0; Mismatches 96;
                                                                                                                                                                                                                                                                                                                       Length 285;
                                                                                                                                                                                                                                                                                        Indels
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RESULT 12

Sequence 6, Application US/09081395 Patent No. 6083746

GENERAL INFORMATION: APPLICANT: Gudkov

Gudkov, Andrei Kazarov, Alexander

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RESULT 13
US-09-081-395-6
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIA Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/09/081,167A
FILING DATE: 18-MAY-1998
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SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Methods for Identifying Genetic
TITLE OF INVENTION: Suppressor Elements and Genes Associated with
TITLE OF INVENTION: Growth in Cancer Cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
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                                                                                                                                           184
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                                                                                                                                                                                                                                               105 ATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGCTGGTGCT 164
                                                                                                                                                                                                                                                                                    64 GTCGCGGACATCGGACTGGCCGCCTGGGGACGGAAGGCTCTGGATATAGCTGAGAATGAG 123
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: No. 6083745nan, Kevin REGISTRATION NUMBER: 35,303 REFERENCE/DOCKET NUMBER: 93
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CLASSIFICATION:
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STATE: Illinois
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les 126; Conserv
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                                                                                                           GCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTAC 266
                                                                                                                                           CGCATTGCTGGCTGCCCATGACCGTGGAGACTGCTGTTCTCATTGAGACTCTCGTG
                                                                          GCCCTGGGTGCTGAGGCGCGGTGGTCCAGCTGCAACATCTTC 285
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300 S. Wacker Drive, 32nd Floor
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                                                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 3.4e-13;
0; Mismatches 96;
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US-09-416-833榮6
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                                                                                                                                 Sequence 6, Application US/09416833 Patent No. 6197521
                                                                                                                   GENERAL INFORMATION:
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                                                                                     APPLICANT:
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LENGTH: 285 base pairs
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MEDIUM TYPE: Floppy disk
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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NUMBER
                                                                        APPLICANT:
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            TITLE OF INVENTION:
                                                         APPLICANT:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                       Roninson,
                                                                       Mazo, Ilya
                                                                                   Kazarov, Alexander
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Suppressor Elements and Genes As
Growth in Cancer Cells
           , Igor B
Methods for Identifying
Suppressor Elements and
Growth in Cancer Cells
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Pred. No. 3
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Genes Associated with Malignant
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PCT-US95-02521-6
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GENERAL INFORMATION:
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Best Local Similarity
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                                                                         TITLE OF INVENTION: Methods
TITLE OF INVENTION: Suppress
TITLE OF INVENTION: Growth 1
NUMBER OF SEQUENCES: 13
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MEDIUM TYPE: Floppy disk
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                                           COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                               SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTCGCGGACATCGGACTGGCCGCCTGGGGACGGAAGGCTCTGGATATAGCTGAGAATGAG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTGAAGAACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCCAAGAC 104
                                                                                                                                                                                                                                                                                                                                    GCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTAC 266
                                                                                                                                                                                                                                                                                                                                                                       CGCATTGCTGGCTGCCCATGACCGTGGAGACTGCTGTTCTCATTGAGACTCTCGTG
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               APPLICATION DATA:
                                                                                                                                                                                                                    Application PC/TUS9502521
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                               PatentIn Release #1.0, Version #1.25 (EPO)
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                                                                                                                              Methods for Identifying
Suppressor Elements and
Growth in Cancer Cells
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PCT/US95/02521
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Pred. No. 3.4e-13;
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Genes Associated with Malignant
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FILING DATE:

INFORMATION FOR SEQ ID NO: 6

SEQUENCE CHARACTERISTICS:

LENGTH: 285 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
PCT-US95-02521-6
                                                                                                                                                                                                                                                                                                     &
Search completed: April 21, 2003, 04:01:49 
Job time: 24.6401 secs
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Best Local Similarity 56.8%;
Matches 126; Conservative
                                                                          105 ATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAAGCCCTTGGCTGGTGCT 164
                                                                                                             225 GCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTAC 266
                                                                                                                                                  184 CGCATTGCTGGCTGCCCTGCGCATGACCGTGGAGACTGCTGTTCTCATTGAGACTCTCGTG 243
                                                                                                                                                                        124 ATGCCAGGGTTGATGCGCATGCGGGAGATGTACTCAGCCTCCAAGCCACTGAAGGGTGCT 183
                                                                                                                                                                                                                                                                                                                           45 GTGAAGAACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGAC 104
                                                                                                                                                                                                                                                                                                   64 GTCGCGGACATCGGACTGGCCGCCTGGGGACGGAAGGCTCTGGATATAGCTGAGAATGAG 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6:
                                                                                                                                                                                                                                                                                                                                                                            Score 68.4; DB 5;
pred. No. 3.4e-13;
0; Mismatches 96;
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Minimum DB
Maximum DB
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No.
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OM nucleic -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                          Score
    106.8
97.2
94.6
87.4
68.4
52.6
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seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            April 21, 2003, 02:39:45; Search time 83.4703 Seconds (without alignments) 5018.577 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             639749 seqs, 502280978 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Published_Applications_NA: *
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
'cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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                                                                                             10 US-09-966-881-9
9 US-10-037-598-26
9 US-09-754-853A-4
9 US-09-746-660A-101
9 US-09-738-626-836
9 US-09-746-660A-97
10 US-09-960-352-10073
9 US-09-738-626-837
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                                                                              US-09-960-352-4421
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Sequence 10073, A
Sequence 837, App
Sequence 117, App
Sequence 4421, Ap
Sequence 1, Appl1
Sequence 6, Appl1
Sequence 6, Appl1
Sequence 11499, A
                                                                                                                                       Sequence 101, App
Sequence 836, App
Sequence 97, Appl
Sequence 10073, A
                                                                                                                                                                                                                                                                                                                                                                                                          Description
                                                                                                                                                                                                                        Sequence
Sequence
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Sequence 850, App
Sequence 439, App
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Sequence 344, App
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26, Appl
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29.8	29.8	30	30.2	30.4	30.4	30.6	30.6	30.6	30.6	30.8	31	31.6	31.6	32.8	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	33.6	35.6	42.8
7.1														7.9		Ļ	Ļ	ï	Ë	Ļ	8.1	Ļ	Ļ	'n	10.3
750	750	1878	1317	3507	3507	1560	1473	1274	594	457	3306	8670	8670	53522	26018	26018	26018	26013	26013	26013	26006	26006	26006	99	110
9	9	φ	9	10	10	ģ	9	9	10	10	9	10	10	9	10	10	9	10	10	9	10	10	φ	10	9
US-10-184-634-104	US-10-184-644-104	US-09-738-626-3457	US-10-121-032-2	US-09-834-975-838	US-09-834-975-829	US-09-995-898A-28	US-09-995-898A-3	US-10-085-188-1	US-09-864-761-7563) US-09-969-708-369													
Sequence 104, App	Sequence 104, App	Sequence 3457, Ap	Sequence 2, Appli	Sequence 838, App	Sequence 829, App	Sequence 28, Appl	Sequence 3, Appli	Sequence 1, Appl1	Sequence 7563, Ap	Sequence 515, App	Sequence 7, Appli	Sequence 369, App	Sequence 103, App	Sequence 1, Appli	Sequence 1637, Ap	Sequence 1962, Ap	Sequence 1962, Ap	Sequence 1636, Ap	Sequence 1961, Ap	Sequence 1961, Ap	Sequence 1638, Ap	Sequence 1963, Ap	Sequence 1963, Ap	Sequence 209, App	Sequence 179, App
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ALIGNMENTS

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US-09-782-051-1
                                                                                                                                                                                                                         Matches 417; Conservative 0; Mismatches 17: DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION: APPLICANT: Hart, De
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Patent No. US20020035078A1
                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 2563
TYPE: DNA
ORGANISM: HOMO SAP16
FEATURE:
NAME/KEY: CDS
LOCATION: (3)..(1847
OTHER INFORMATION: 0
OTHER INFORMATION: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hart, Derek N J
TITLE OF INVENTION: Enzyme having S-adenosyl-L-homocysteine hydrolase
TITLE OF INVENTION: (ARCY) type activity
FILE REFERENCE: 24305 MRB
CURRENT APPLICATION NUMBER: US/09/792,051
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: PCT/N297/00133
PRIOR FILING DATE: 1997-10-06
PRIOR APPLICATION NUMBER: NZ 299507
PRIOR FILING DATE: 1996-10-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Open reading frame extends without a stop OTHER INFORMATION: for the full 5' nucleotide sequence. The OTHER INFORMATION: initiation codon has yet to be identified
                                                                                                                                             529 GAGAGAAGCAACCCAACTCCAAGGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGC 588
121 CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA 180
                                                589
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                                                                                                AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 120
                                                AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 648
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; LOCATION: (1)...(636)
; OTHER INFORMATION: n = A,T,C or
US-09-879-536-850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/879,536
CURRENT FILING DATE: 1908-109-21
PRIOR APPLICATION NUMBER: US 60/088,801
PRIOR FILING DATE: 1998-06-10
NUMBER OF SEC. 15
                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQ ID NOS: 850
SOFTWARE: FastSEQ for Windows Version 3.
SEQ ID NO 850
LENGTH: 636
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-879-536-850/c
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                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens
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                                                                                                                                                                    179 TACACACATCACAGCCCAGACAGC-GGTGTTGATTGAGACACTCTGTGCCCTGGGGGGCTC 237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      649 CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA
 358 GTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGG
                                                     298 CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGT 357
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US20υ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGG 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGG 417
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                                                                                                     AGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG
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                                                                                                                                                                                                                                        238;
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Monahan, John E.
Schlegel, Robert
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Catino, Theodore J.
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US-09-925-301-217

GENERAL INFORMATION: Sequence 217, Patent No.

US20020052308A1

Application US/09925301

APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10

SEQ ID NO 217

ENGTH: 2200

TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:

NUMBER OF SEQ ID NOS: 1694 SOFTWARE: PatentIn Ver. 2.

PRIOR APPLICATION NUMBER: PCT/US00/05882 PRIOR FILING DATE: 2000-03-08 PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12

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US-09-925-300-439
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; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (688)
; OTHER INFORMATION: n equals a,t,g,
US-09-925-300-439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 439
LENGTH: 721
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                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05988
PRIOR FILING DATE: 2000-03-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Craig Rosen, APPLICANT: Steve Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/925,300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Nucleic Acids, Proteins FILE REFERENCE: PA101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          592 AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT
                                                                       652
                                  181 CACACATCA 189
                                                                                                        121 CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA 180
                                                                                                                                                                                                                  532 GAGAGAAGCAACCAACTCCAAGGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGC 591
                                                                                                                                                                                61 AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 120
                                                                                                                                                                                                                                                    1 GAGAGAAGCAGCAAACCAACTCCAAGGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGC 60
CACATTACA 720
                                                                       CACTCAGGAAACGTGCTCAGGGGGARAAG
                                                                                                                                                                                                                                                                                        178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Steve Ruben
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                         42.7%;
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                                                                                                                                                                                                                                                                                                         Score 178; DB 10;
Pred. No. 1.3e-50;
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RESULT 5
US-10-044-090-344
; Sequence 344, Application US/10044090
; Patent No. US20020137081A1
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                                                                                                                                                                                                                                                  ; OTHER INFORMATION: Incyte ID No. US20020137081A1 1468237CB1
US-10-044-090-344
                                                                                                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 200:
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 344
LENGTH: 2429
                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/10/044,090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION FILE REFERENCE: PA-0028 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Olga Bandman
                                                                                                                                                                                                                                                                                    FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
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LOCATION: (2188)
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                                                                    112 CTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAG 171
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292 CACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGCGCGAGTCAGAAGATGACTTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               168 GCCTGATGCGTATGCGGGAGCGGTACTCGGCCTCCAAGCCACTGAAGGGCGCCCCGCATCG
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                                                                                                                                                                      J2.9%;
Local Similarity 60.9%;
es 220; Conservation
                                                                                                                                         52 ACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTG 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       52 ACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTG 111
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les 223; Conserv
                                   GCCTGATGCGTATGCGGGAGCGGTACTCGGCCTCCAAGCCACTGAAGGGCGCCCGCATCG
                                                                                                       ACATCGGCCTGGCTGCCTGGGGACGCAAGGCCCTGGACATTGCTGAGAACGAGATGCCGG 167
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                                                                                                                                                                                              Score 137.2; DB 12; Pred. No. 1.8e-36;
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Pred. No. 1.7e-36;
0; Mismatches 143;
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                                            US-09-966-881-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9, Application US/09966881
Patent No. US20020120960A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION: TELEPHONE: (302) 886-1699 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     468 ACGGGG 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/242,860
FILING DATE: 29-Mar-1999
APPLICATION NUMBER: GB 9618862.8
FILING DATE: 10-SEP-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Zeneca Ag Products
STREET: 1800 Concord Pike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medina-Suarez, Rosybel
TITLE OF INVENTION: Genetic control Of Fruit Ripening
NUMBER OF SEQUENCES: 57
                                                                                                                         MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
                                                               SEQUENCE DESCRIPTION:
                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Seymour, Graham
                                                                                                        IMMEDIATE SOURCE
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                                                                                                                                                             LENGTH: 793 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/966,881 FILING DATE: 28-Sep-2001
                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: SEE 50183/UST
                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: GB 9708366.1 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STATE: DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Wilmington
                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 08-SEP-1997
                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 25-APR-1997
APPLICATION NUMBER: PCT/GB97/02424
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                                                               SEQ ID NO:
                                                                                                                                                                                                                                                                      886-1699
                                                                                                                                                                                                                                                                                                                             L1za D.
R: 33,712
  Score 114.4;
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Query Match

27.48;

DB 10;

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; SEQ ID NO 26
; LENGTH: 3830
; TYPE: DNA
; ORGANISM: Glycine max
US-10-037-598-26
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US-10-037-598-26
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Delanney, Xavier
TITLE OF INVENTION: Soybean Plants with Enhanced Yields and Methods for Breeding
TITLE OF INVENTION: Screening of Soybean Plants with Enhanced Yields
FILE REFERENCE: 38-21(52175)B
CURRENT APPLICATION NUMBER: US/10/037,598
CURRENT FILLING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 06/260,040
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Monsanto Co
APPLICANT: Concibido,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn version 3.0
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                                                                                    198
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             258 AACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTGCAGTG 317
                                                                                                                                                                                                                                78
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nes 202; Conservative
                                                                                                                                                                                                                                                                                                        GCGAGTACAAGGTGAAGGACCTTTCTCAGGCTGACTTCGGCCGCCTCGAGATCGAGCTGG 141
                                                                                                                                                          CGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCT 137
                                                                                                                                                                                                                                                                      AAAACCACGAGTGGTCGCGAGTACAAGGTCAAGGACCTTTCCCAGGCCGACTTCGGCCGC 1812
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTC 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCGCCGGCGCCCCCATCCCGGCTCCCTCCACATGACCATCCAGACCGCCGTCCTCATCG
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                                                  ACCGCCGTTCTCATTGAGACCCTCACCGCCCTTGGCGCCGAGGTCCGCTGGTGCTCCTGC 1992
                                                                                    ACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGGACCACGCCGCTGCCGCCATTGCCCGCCGACTCCGCCGCCGTCTTCGCCTGGAAGGGAG
                                                                                                                          Concibido, Vergel
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57.1%;
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0; M1smatches 146;
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Pred. No. 1.3e-28;
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179927 TGGG 179924
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Best Local Similarity
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CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
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APPLICANT: Parsons, Jeremy D.
APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Soybean Cyst Nematode
FILE REFERENCE: 38-10(15810)B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 1119
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LOCATION: (1)..(513509)
OTHER INFORMATION: unsure at
OTHER INFORMATION: Clone ID:
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LOCATION: (111805)..(113968),(114684)..(115204)
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                                                                                                   258 AACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTGCAGTG 317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTCGCTTGGAAGGCCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTGTGAAC 377
                                                                                                                                                     ACCGCCGTTCTCATTGAGACCCTCACCGCCCTTGGCGCCGAGGTCCGCTGGTGCTCCTGC 180048
                                                                                                                                                                                                                                                      CTCGAGATCGAGCTGGCCGAGGTTGAGATGCCCGGCCTCATGGCCTGTCGGACCGAGTTC 180168
                                                                                                                                                                                                                                                                                                                                                                                                        CGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTG¢T 137
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                                                                                                                                                                                  ACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGT 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                208; Conservative
                                                    AACATCTTCTCCACCCAGGACCACGCCGCCGCCGCTATTGCCCGCGACAGTGCCGCCGTC 179988
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US-09-746-660A-101
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Best Local Similarity
Matches 225; Conserv
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SEQ ID NO 101
LENGTH: 1396
TYPE: DNA
ORGANISM: Corynebacterium glutamicum
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ITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
ITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ILE REFERENCE: BGI-121CP2
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                                                                                                                                                                                                                                                         263 CACATGACGGTCCAGACCGCCGTGCTTATTGAGACCCTCACTGCTTTGGGCGCTGAGGTT 322
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                                                                                                                                                                                                                                                                                                                                                                                  123 CTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACA 182
443 CTGGAGGAGTACTGGTGGTGCATCAACCAGATCTTCAGCTGGGGCGATGAGCTGCCAAAC 502
                                   183 CACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCCTGGGGGGCTCAGTGC 242
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OR APPLICATION NUMBER: 09/606740
OR FILING DATE: 2000-06-23
OR APPLICATION NUMBER: 09/603124
OR FILING DATE: 2000-06-23
OR APPLICATION NUMBER: 60/141031
OR FILING DATE: 1999-06-25
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FILING DATE: 2000-03-09
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FILING DATE: 1999-08-12
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                                                                               GGCTCCGGCACCGTCGAAGAGCCAGCTGGTGTTCCCAGTATTCGCGTGGAAGGGTGAGTCA 442
                                                                                                                                                                     CGTTGGGCTTCCTGCAACATTTTCTCCACCCAGGATGAGGCTGCAGCGGCTATCGTTGTC 382
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                                                                                                         --AGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCA 338
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Pred. No. 2.5e-28;
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RESULT 11
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RESULT 10
US-09-738-626-836
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US-09-738-626-836
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LENGTH: 1422
TYPE: DNA
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Best Local Similarity
Matches 225; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: JP 00/280988 PRIOR FILING DATE: 2000-08-03 NUMBER OF SEQ ID NOS: 7059
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PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
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                                                                                                                                                                                             301
                                                                                                                                                                                                                              211
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391 ATGATCCTCGACGACGGCG 409
                                   399 ATGATCCTGGATGATGGGG 417
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                                                                         CTGGAGGAGTACTGGTGGTGCATCAACCAGATCTTCAGCTGGGGGGATGAGCTGCCAAAC
                                                                                                                                                                                                                            CGTTGGGCTTCCTGCAACATTTTCTCCACCCAGGATGAGGCTGCAGCGGCTATCGTTGTC 270
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OCHIAI, KEIKO
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TATEISHI, NAOKO
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US-09-746-660A-97
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: LOCATION: (101)..(1534)
: OTHER INFORMATION: RXN00132
US-09-746-660A-97
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Best Local Similarity
Matches 225; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn
SEQ ID NO 97
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CURRENT APPLICATION NUMBER: U$/09/746,660A
CURRENT FILING DATE: 2000-12-22
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APPLICANT: Kroger, Burkhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: 09/606740 PRIOR FILING DATE: 2000-06-23
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ITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
ITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENGTH: 1557
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                                                                                                                                                                                                                                                                               243 CGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTG-- 300
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                  399 ATGATCCTGGATGATGGGG 417
                                                                                                      383 GGCTCCGGCACCGTCGAAGAGCCAGCTGGTGTTCCAGTATTCGCGTGGAAGGGTGAGTCA
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FILING DATE: 2000-03-09
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/142101 FILING DATE: 1999-07-02
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Schroder, Hartwig
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Pred. No. 2.6e-28;
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LOCATION: (284),(292)
; OTHER INFORMATION: unsure at all n locations
; OTHER INFORMATION: Clone ID: 43-LIB34-036-Q1-E1-C4
US-09-960-352-10073
                                                                                                                                                                                                                                                                                                                                                                      RESULT 13
US-09-738-626-837/c
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SEQ ID NO 10073
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                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                           Sequence 837, Application US/09738626 Publication No. US20020197605A1
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Best Local Similarity 61.1%;
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                                    FILE OF INVENTION: NOVEL POLYNUCLEOTIDES
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                                                                                                                      YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
                                                                                                                                                                                                                                                                                  NAKAGAWA, SATOSHI
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LICATION NUMBER: US/09/738,626 ING DATE: 2000-12-18
                                                                                                                                                                                      HAYASHI, MIKIRO
OCHIAI, KEIKO
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                                                                               OZAKI, AKIO
                                                                                                                                                                                                                                                             MIZOGUCHI,
                                                                                                      IKEDA, MASATO
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Pred. No. 6.4e-27;
0; Mismatches 110;
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; LENGTH: 708
; TYPE: DNA
; ORGANISM: Corynebacterium glutamicum
US-09-738-626-837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
     APPLICANT: Hurban, Patrick
TITLE OF INVENTION: Expressed Sequences of Arabidopsis
TITLE OF INVENTION: thalfana
FILE REFERENCE: 2024 (PARA-013PRV)
CURRENT APPLICATION NUMBER: US/09/770,149
CURRENT FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117, Application US/09770149
Patent No. US20020059663A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                           APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 ---AGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        358 GTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    526 TTTTCTCCACCCAGGATGAGGCTGCAGCGGCTATCGTTGTCGGCTCCGGCACCGTCGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262 TCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTG------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          586 CCGTGCTTATTGAGACCCTCACTGCTTTGGGCGCTGAGGTTCGTTGGGCTTCCTGCAACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                646 ACGAGCAGCCTTTGAAGGGCGCCCGAATTGCTGGTTCTATCCACATGACGGTCCAGACCG
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                An, Yong-Qiang
Hamilton, Carol M.
Price, Jennifer L.
Raines, Tracy M.
                                                                                                      Hoffman, Neil
Hurban, Patrick
                                                                                                                                          Davis, Keith R.
Allen, Keith
                                                                                                                                                                              Kricker, Maja
Slader, Ted
                                                                                                                                                                                                                  Garcia, Carlos A.
                                                                                                                                                                                                                                   Woessner, Jeffrey P. Haas, William David
                                                                                                                                                                                                                                                                   Matthew, Abraham
Ledford, Brooke
                                                                                                                                                                                                                                                                                                                                                  Yu,
                                                                                                                                                                                                                                                                                                           Page, Amy
                                                                                                                                                                                                                                                                                                                            Rameaka, Joshua G.
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Pred. No. 2.5e-26;
0; Mismatches 12;
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; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 19-LIB34-025-Q1-E1-E3
US-09-960-352-4421
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US-09-960-352-4421
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-770-149-117
                                                                                                                                                                                                                                                       SEQ ID NO 4421
LENGTH: 433
TYPE: DNA
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SEQ ID NO 117
LENGTH: 728
                                                                                                                       Matches
                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 4421, Application US/09960352 Patent No. US20020137139A1
                                                                                                                                                                                                                                                                                                             APPLICANT: Mathialagan, Nagappan
TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED
TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION
FILE REFERENCE: 16511.006/37-21(10298)C
CURRENT APPLICATION NUMBER: US/09/960,352
CURRENT FILING DATE: 2001-09-24
NUMBER OF SEQ ID NOS: 15112
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Best Local S
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NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Warren, Wesley C.
273 CAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGC
                                                                           213 GAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTACTCAACT 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 TTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTGTATTGACCGCTGTGTGAAC 377
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   198 ACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGGCTCAGTGCCGCTGGTCTGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   382 CTCGAACTCGAGCTCGCCGAAGTTGAGATGCCTGGACTCATGGCTTGTCGTACCGAATTC
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                                           37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             262 ACCGCCGTACTCATCGAAACCCTAACTGCTCTCGGTGCTGAAGTCAGATGGTGTTCCTGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    82
                                                                                                                     Local Similarity 66.:
es 136; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         78 CGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCT 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GAGACCCTCGTTGCCCTGGGTGCTGAGGTGCGGTGCTCCAGCTGCAATATCTTCTCCACC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TGGGGT 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TTCGCCTGGAAAGGTGAGACTCTTCAGGAGTACTGGTGGTGTACCGAGCGTGCTCTAGAT 83
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Byatt, John C.
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; Pred. No. 2.9e
0; Mismatches
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Pred. No. 4.7e-23;
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nes 69;
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Search completed: April 21, 2003, 07:21:15 Job time: 336.47 secs

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Maximum DB
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Gapop 10.0 , Gapext 1.0
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11996.532 Million cell updates/sec
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Copyright (c) 1993 - 2003 Compugen Ltd.
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gb_est2:*
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BG706498 602670053
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                                                                                                                         Description
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COMMENT
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KEYWORDS
SOURCE
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Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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                                                                                  Helix Research Institute
1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                                                                                                                                                                                                                                 Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1. (bases 1 to 700)
Email: genomics@hri.co.jp
HRI human cDNA project; 5'-& 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                 Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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K-EST0026 7h07e06.x NV724011 603251755 603194678 0P2.0.231 601179921

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01-AUG-2002 , |mRNA

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     http://mage.llnl.gov
Plate: LLCM1797 row: 1 column:
High quality sequence stop: 728.
Location/Qualifiers
                                                                                                                                   Contact: Robert Strausberg, |
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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Mammalia; Eutheria;
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/note="Vector: pME18SFL3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
1 (bases 1 to 744)
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI),
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL
DNA Sequencing by: Incyte Genomics, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                mRNA sequence.
BG699160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BG699160 744 bp m 602678818F1 NIH_MGC_95 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                       NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection
                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BG699160.1
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/tlssue_type="rhabdomyosarcoma"
/tlssue_type="rhabdomyosarcoma"
/lab_host="PH10B (phage-resistant)"
/lab_host="Ph10B (phage-resistant)

/lab_host="Ph10B (phage-
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/db_xref="taxon:9606"
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Primates;
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Pred. No. 2.4e-110;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mRNA
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REFERENCE
AUTHORS
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ORGANISM
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VERSION
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                                                                                                                                                   DEFINITION
                                                                                              KEYWORDS
TITLE
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                                                                                                                                                                                                                                                                                          AGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCCAGTCAGAAGATGACTTCTGGTGGTGTA
                                                                                                        mRNA sequence.
BG706498
BG706498.1 GI:13981903
                                                                                                                                                BG706498 763
602670053F1 NIH_MGC_96 Homo
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Location/Qualifiers
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                                                                 Homo sapiens
 National Institutes of Health,
              Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 763)
NIH-MGC http://mgc.nci.nih.gov/.
                                      Eukaryota; Metazoa;
Mammalia; Eutheria;
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/clone_11b="NIH_MGC_95"
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/lab_host="DH10B"
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                                        Chordata;
Primates;
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Pred. No. 2.4e-110;
; Mismatches 0;
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                                        Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
 Mammalian Gene
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IMAGE:4792813 5',
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417; Conserv
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AU126038
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Tissue Procurement: Miklos Falkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI)
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
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Contact: Robert St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://image.llnl.gov
Plate: LLAM10671 row: j column:
High quality sequence stop: 737.
AU126038
                    sequence
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                                           NT2RM4 Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:4792813"
/clone_lib="NIH_MGC_96"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="hypothalamus"
/lab_host="DH10B"
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Pred. No. 2.4e-110;
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Best Local Similarity 100.0%;
Matches 417; Conservative 0
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Eukaryota; Metazoa; Chordata; Cr
Mammalia; Eutheria; Primates; Ca
1 (bases 1 to 764)
Ota, T., Wakamatsu, A., Ozawa, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: genomics@hri.co.jp
HRI human cDNA project; 5'- 6 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
Location/Qualifiers
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1532-3 Yana, Kisarazu, Chiba
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Contact: Takao Isogai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S., Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzuki
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81-438-52-3986 -
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precursor cells"
157 c 228 g 183 t
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/db_xref="taxon:9606"
/clone="NT2RM4002613"
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/cell_line="NT2"
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Pred. No. 2.4e-110;
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372 CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA
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             AGGCTGGAGTTGCAGTGTTCGCCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTA
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Clone distribution: MCC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov; n. column: 03
plate: LLAM10711 row: n. column: 03
High quality sequence stop: 707.
Location/Qualifiers
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Tissue Procurement: Miklos Palkovits,
cDNA Library Preparation: Michael J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Toshiyuki and Piero Carninci (RIKEN) cDNA Library Arrayed by: The I.M.A.G.E.
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
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National Institutes of Health, Mammalian
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ilarity 100.0%;
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/clone="IMAGE:4815170"
/clone_11b="NIH_MGC_95"
/tissue_type="hippocampus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      organism="Homo sapiens"
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Pred. No. 2.5e-110;
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Brownstein
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	PECTE	DAGCCCAG DAGCCCAG	ACGTGCT ACGTGCT	TGGACGC	GCAAACC GCAAACC	Va	a 201	Plate: LLAW12206 High quality seq Location 1867 /organit /clone- /clone- /clone- /lab_hos /note- % Site_2: Average	Lissue Frocurement: A CDNA Library Prepara CDNA Library Arrayed DNA Sequencing by: A Clone distribution: I found through the I.M found through the I.M	Mammalia; Eutheria; Primates 1 (bases 1 to 867) NIH-MGC http://mgc.nci.nih.go National Institutes of Healt Unpublished (1999) Contact: Robert Strausberg, Contact: Robert Strausberg, Contact: Robert Strausberg,	2 9 4	TGTGAAC TGTGAAC
1111111	PAACATCI	ACAGCGG ACAGCGG	CAGGGGG	CGGGAGA CGGGAGA	AACTCCA AACTCCA	100.0%; 100.0%; Live 0;	201 c	wil2206 row: 1 try sequence structs sequence structor qualif867 dorganism="momo dorganism="mage:5" (clone="iMage:5" clone="ib="nim" rissue_type="midte" libe_1: Sali; C. lite_2: Sali; C. verage insert	reparat reparat rrayed by: Ag tion: M	867) 867) mgc.nci utes of 99) Straus	02958 NIH_M uence. GI:18502949	ATGGATG
	ACTCAAC	TGTTGAT	AGAAGCC AGAAGCC	TTGAGAT	AGGGCAG AGGGCAG	Score Pred.	241 g	Plate: LLAM12206 row: 1 column High quality sequence stop: 670. Location/Qualifiers 1867 /organism="Homo sapiens" /db_xrefs="taxon:9606" /clone="IMAGE:5528995" /clone=1h="MAGE:5528995" /clssue_type="melanotic" /lab_host="DH10B (phage:/note="Organ: skin; Vectsite_2: Sali; Cloned uni average insert size 2 kh	TISSUE FIGUREMENT: ANCOPORTY CDNA Library Preparation: Life F CDNA Library Arrayed by: The I.M DNA Sequencing by: Agencourt Bio Clone distribution: MGC clone di found through the I.M.A.G.E. Cons	eria; Primates; (867) /mgc.nci.nih.gov, tutes of Health, 999) t Strausberg, Ph t Strausberg, Ph	867 _72	GGTGGCA GGTGGCA
	TCAGAATO	TGAGACA(TGAGACA(CTTGGCTC	TGCAGAGO TGCAGAGO	CAGCAATS CAGCAATS	ore 417; DB 13; ed. No. 2.6e-110; Mismatches 0;	202 t		fe Techr I.M.A.(Bioscie e distri	; Catarrhini; jov/. h, Mammalian Ph.D.	bp mRNA HOmo sapie	GCCAAC? GCCAAC?
	SAAGTAGO SAAGTAGO	OTCTGTGC	GIGCIA:	AAGACAT AAGACAT	TCTGTGI		Ľ	: 20 melanoma " resistant) " (cor: pCMV-SP(ldlrectional) ddlrectional) b. Library	nologies 3.E. Con ance Cor bution lum/LLNI	_		TGATCCT
	GCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAAGT	CACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGT 	CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA 	AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 	GAGAGAAGCAGCAAACCAACTCCAAGGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGC 	Length 8	1 others	d 19	cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can cound through the I.M.A.G.E. Consortium/LLNL at:	Hominidae; Home	linear EST'05-FEB-20 s CDNA clone IMAGE:552899 Vertebrata; Euteleostomi;	TTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGAGGG
111111	CIGGCIG CIGGCIG	GCTCAGT GCTCAGT	GGCTGTA GGCTGTA	CTGATTT CTGATTT	ATCAAGC ATCAAGC	867; 0; Ga			(LLNL) n tion car	Homo	Eutelec	3GGG 417 3GGG 668
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	D Q	Оу 1 рь 6	Qy 1 Db 5	Qy . 5	Qy Db 4	Query Best Match	BASE CO		FEATURE SO	ORGANISM REFERENCE AUTHORS TITLE JOURNAL	RESULT 8 AL551097 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	Db 5 Qγ . 3 Db 5
		81 CACA 41 CACA	21 CACT	61 AGGC 21 AGGC	1 GAGA []]] 61 GAGA	Match Local es 41	TNDC	_	s		S ION	02 AGGC
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	SCTTGTAP	3CCCAGAC 3CCCAGAC	ACTOSTSC 	3GACGCCG 3GACGCCG	DAAACCAA DAAACCAA	vai	231 c	/db_xref="taxon:9666" /dlone="cS0D1066YM07" /clone="type="FITI INF1006, PL2" /fissue_type="placenta" /	ye - Centre National de : 91006 EVRY cedex - France segref@genoscope.cns.fr, Location/Qualifiers 1 921	o sapiens aryota; Metazoa; malia; Eutheria; (bases 1 to 921) W.B., Gruber,C., 1-length cDNA 111 blished (2001)	₽::	CAGTGTT TGAACAT
11111	CATCTAC	AGCGGTG AGCGGTG	GGGGGAG 	GGAGATT	CTCCAAG CTCCAAG	.0%;	c 30	db_xref="taxon:9606" (dlone="CSU01066YM07" Clone="tb="LFI kFL00" Clone=tb="LFI kFL00" Clone=type="placent" note="Vector: pCMVSp" as primed with a Not nriched double-stra lioned into the Not I cector: Library was n ife Technologies: Co ife Technologies: Co cockville, Maryland 2 mail: fliang@ilfete		a; Chordata; a; Primates; 1) ., Jessee,J. libraries an	PL2	CGCTTGG; GGATGGG; GGATGGG;
111111	TCAACTC	TTGATTG! TTGATTG!	AAGCCCTS AAGCCCTS	GAGATTGO GAGATTGO	GGCAGCAC GGCAGCAC	core 417 red. No Mismato	302 g	9606 " 6YM07 " 6YM07 " NFL006	nal de s - France cns.fr, iers	Chordata; Ci Primates; Ci Jessee, J. an Draries and r	921 bp Homo sap	AAGGGCG <i>F</i> IGGCAGGC
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lst strand cDNA five prime end with Not I and the pCMVSPORT 6 s constructed by fer Technologies, or bive 01 610 8371	Contact: Genoscope Genoscope - Centre National de Sequencage Bp 191 91006 EVRY cedex - France Email: seqref@genoscope.cns.fr, Web : www.genoscope Location/Qualifiers 1. 921 /organism-"Homo sapiens" /db_xref-"taxon:9606" /clone-"ScOpio66xW07" /clone-"ScOpio66xW07" /clone-"FCSOpio66xW07" /clone-"FCSOpio66xW07" /clone-"Lib-"LTI_NFL006_PL2" /tissue_type-"Placenta" /note-"Vector: pCMVSPORT 6; Site_1: Not1; was primed with a NotI-oligo(dT) primer. enriched, double-stranded cDNA was digeste cloned into the Not I and Eco RV sites of vector: Library was normalized. Library wa Life Technologies. Contact: Feng Liang Lia Life Technologies. Contact: Feng Liang Lia a division of Invitrogen 9800 Medical Cent Rockville, Maryland 20850, USA Fax: (1) 3 Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com" 217 a 231 c 302 g 170 t 1 others	EATURES SOURCE
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1 (bases 1 to 944)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
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Plate: LLAM9598 row: k column: 18
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Tissue Procurement: DCTD/DTP
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Contact: Robert Strausberg, Ph.D.
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Clone distribution: MGC clone distribution information can
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//lab_host="DH108 (phage=resistant)"
//note="Organ: ovary; Vector: pcMV-SPORT6; Site_1: NotI;
//note="Organ: ovary; Vector: pcMV-SPORT6; Site_1: NotI;
//site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
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Tissue Procurement: ATCC
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection
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/db_xref="taxon:9606"
/db_xref="taxon:9606"
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/lab_host="D10B (phage-resistant)
/note="organ: testis; Vector: pCMV-SPORT6; Site_1: Not1;
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Average insert size 2.5 kb. Library enriched for full-length clones and constructed by Life Technologies.
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 300
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Db 421	QY 241 GCCGCTGGTCTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTG 300
Qy 181	Db 476 CACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGGCTCAGT 535
Db 361	Qy 181 CACACATCACAGCCGCAGACAGCGGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGT 240
Оу 121 /	Db 416 CACTCAGGAAACGTGCTCAGGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA 475
Db 301	Qy 121 CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA 180
ОУ 61	Db 356 AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 415
Db 241	Qy 61 AGGÇAGAATTTGGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 120
Qy 1	Db 296 GAGAGAAGCAACTCCAAGGGCAGCAGCAGTTTCTGTGTGAAGAACATCAAGC 355
Best Loca Matches	OY 1 GAGAGAAGCAACCAACTTCCAAGGGCAGCAGCAATTTTCTGTGTGAAGAACATCAAGC 60
BASE COUNT	cal Similarity 99.8%; Score 416.6; DB 9; Length 858;
	BASE COUNT 212 a 206 c 255 g 182 t 3 others ORIGIN
	Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fliang@lifetech.com URL:
	cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by
	/note-"Vector: pcMvSpORT 6; Site_1: NotI; lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was didested with Not I and
٠	/clone_lib="LTI_NFL006_PL2" /tissue_type="placenta"
	/db_xref="taxon:9606" /clone="CS0D1087x118"
Source	/Organism="Homo sapiens"
FEATURES	Location/Qualifiers
,)06 EVRY cedex – Fran Tref@qenoscope.cns.fr
COMMENT	COMMENT Contact: Genoscope Genoscope - Centre National de Sequencage
JOURNAL	AL.
AUTHORS	(A)
REFERENCE	Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 858)
ORGANISM	W. Homo sapiens
VERSION KEYWORDS	VERSION AL554850.1 G1:12896025 KEYNORDS EST.
ACCESSION	prime, mRNA sequence. ON AL554850
RESULT 12 AL527928 LOCUS DEFINITION	AL554850 AL554850 AL554850 AL554850 AL554850 AL554850 AL554850 DEFINITION AL554850 LTI_NFL006_PL2 Homo sapiens CDNA clone CS0DI087YL18 5
Db 656	THE TRANSPORTED AND A TRANSPOR
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7 596 gd	Db 385 AGGCTGGAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTA 444
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Db 536 (Db 325 GCCGCTGGTCTGCTTGTAACRCTACTCAACRCTAGTAACCTGCAGCACTGCAGCACTGCAGCACTGGCTG 384

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CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA 180
                                                                                                                                                                                                    CACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGGCTCAGT 480
                                                                                               CACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTA 420
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                                              CACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGGCTCAGT 240
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AL527928 LTI_NFL003_NBC3 Homo sapiens cDNA clone CS0DC027YC19 5
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BP 191 9100 EVRY cedex - France
Bmail: segref@genoscope.cns.fr, Web : www.genoscope.cns.
Location/Qualifiers
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Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 938)
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was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with Not I and
cloned into the Not I and Eco.RV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed
by Life Technologies. Contact : Feng Liang Life
Technologies, a division of invitrogen 9800 Medical Center
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610
8371 Email : filang@lifetech.com URL :
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a 208 c 275 g 212 t
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/db_xref="taxon:9606"
/clone="CSODC027YC19"
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ab_host="DH10B"
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Pred. No. 3.5e-110;
1; Mismatches 0;
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Query Match
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AUTHORS
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ORGANISM
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295
                                                                                      235 GAGAGAAGCAGCAAACCAACTCCAAGGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGC 294
                                         61 AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 120
                                                                                                             GAGAGAAGCAGCAAACCAACTCCAAGGGCAGCAGCAGTTTCTGTGTGAAGAACATCAAGC 60
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  AGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTT 354
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Location/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished (1999)
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Plate: LLAM10676 row: k column: 01
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Clone distribution: MGC clone distribution information can
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                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cgapbs-r@mail.nih.
                                                                                                                                                                                                                                                                               /note-"Organ: brain; Vector: pBluescriptR (modified pBluescript RS+); Site-1: BamHI; Site-2: SAII-XhoI (gtcgag); Oligo-dr primed using primer 5:-TTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the Cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NTH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

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/lab_host="DH10B"
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/clone_lib="NIH_MGC_96"
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/db_xref="taxon:9606"
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                                                                                                                                                                        Score 415.4; DB 12;
Pred. No. 6.7e-110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nlh.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI),
Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL,
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL,
                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11790 row: p column: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B1668412 857 bp m 603292688F1 NIH_MGC_96 Homo sapiens
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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BI668412
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Contact: Robert Strausberg, Ph.D.
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                        ø
                  /note-"Organ: brain; Vector: pBluescriptR (modified pBluescript KS+); Site_1: BamHI; Site_2: Sall-XhOl (gtcgag); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTVN-3', size-selected for average insert size 2.3 kb and normalized to ROT 5. This is a primary library enriched for full-length clones and constructed using the cap-trapper method (Carninci, in preparation). Library constructed by M. Brownstein (NIMH/NHGRI, National Institutes of Health). Note: this is a NIH_MGC Library."

1 208 c 241 g 189 t
                                                                                                                                                                                                                                    /clone="IMAGE:5312133"
/clone_lib="NIH_MGC_96"
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/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                              /db_xref-"taxon
                                                                                                                                                                                                                                                                                                                                              organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                         location/Qualifiers
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Query Match Best Local Similarity Matches 416; Conserv

99.6%;

Score 415.4; Pred. No. 7.5e 0; Mismatches

.5e-110;

DB 13;

Length 857;

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Gaps

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AUTHORS
TITLE
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1042 bp mrNA linear E AGENCOURT_6400881 NIH_MGC_67 Homo sapiens cDNA clone 5', mRNA sequence.

BM449470

BM449470.1 GI:18498510
                                                                                                                                                                                                                                                                     CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC.clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12117 row: m column: 06
High quality sequence stop: 694.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Cr. Mammalia; Eutheria; Primates; Ca 1 (bases 1 to 1042) NIH-MCC http://mgc.nci.nih.gov/. National Institutes of Health, M. Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                     267
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/tissue_type="retinoblastoma"
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Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
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                                                                                                                                                                                                                     organism="Homo sapiens"
db_xref="taxon:9606"
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 99.3%;
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Score 414;
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                                                                                                                                                                                                                     TCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACAC
ACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGG
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Search completed: April 21, 2003, 03:58:56 Job time: 568.956 secs

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76 Sequence 31 Homo sapi 37 Homo sapi 54 Homo sapi 218 Mus muscu

Homo sapien 76 Homo sapi

Searched:

Scoring table:

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Post-processing: Minimum Match 0%
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U82761.1
                                                                                                                              2258 bp mRNA linear PRI 17-DEC-2001
Homo sapiens S-adenosyl homocysteine hydrolase homolog (XPVkona)
1 (bases 1 to 2258)
Cleaver, J.E., Afzal, V., Feeney, L., McDowell, M., Sadinski, W., Volpe, J.P.G., Busch, D.B., Coleman, D.M., Ziffer, D.W., Yu, Y.,
                                   Homo sapiens.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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BC015304
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M61832 Human S-ade
BC010018 Homo sapi
BC011606 Homo sapi
AK097610 Homo sapi
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129093 Mus muscu
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1091636 Drosophila
1003715 Drosophila
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7835 Xenopus L
8 Drosophila
159 Xenopus lae
12668 Drosophil
136 D.melanogas
136 D.melanogas
                                                                                                                                                                                                                                                                      7699 Sequence
8421 Rattus no
4537 Schizosac
2072 S.pombe c
0808 Rattus no
4978 Sequence
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L.donovani Slime mold

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ACCESSION E	GCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTGATTGACCGCTGTGTGAACATG 360	Οy 301 Db 552
RESULT 2, BC007576 LOCUS	ATCTACTCAACTCAGAATGAAGTAGCTGCAGGCTGGAGGCTGGAGTTGCAGTGTTC 300	Oy 241 Db 492
1512	GCGSTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTGCTAAC 240 	Oy 181 o
1452	GGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACACACAC	Qy 121 of the state of the stat
1392	GAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAG 120	Oy 61 o
	TCCAAGGGCAGCAATTTCTGTGTGAAGAACATCAAGCAGGAGAATTTGGACGCCGG 60 	Oy 1 Db 252
1272	Match 100.0%; Score 1296; DB 9; Length 2258; Local Similarity 100.0%; Pred. No. 0; es 1296; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	Query Match Best Local Matches 129
Db 1212 GTA	VYLLPKKWDEYVASIHLPSEDAHLTELTDDQAKYLGLNKNGPEKPNYYRY" 603 a 513 c 542 g 600 t	BASE COUNT ORIGIN
Db 1152 CAC Qy 961 GTA	VMFGGKQVVVCGYGEVGKGCCAALKALGAIYYITEIDPICALQACMDGFRVVKLNEVI RQVDVVITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLRTPELTWERVRSQ VDHVIWPDGKRVVLLAEGRLLNLSCSTVPTFVLSITATTQALALIELYNAPEGRYKQD	
Qy . 901 CAC	AGARANGES HAGARA TYOL HILLY AN HILL HAGARANGE AN HILLY KARANGER HAGARANGE AN HAGARANGE A	
1092	/translation="MATVTKAPKKQIQFADDMQEFTKEPTKTGRRSLSRSISQSSTDS YSSAASYTDSSDDEVSPREKQQTMSKSSNFCVKNIKQAEFGRREIEJAEQDMSALIS TAFFACGFEFTAAFATTACTAVTTFFTCAKGACGGGGCTATTGFTCATTAAAT	
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Oy 781 AAG	/note="xeroderma pigmentosum variant" /codon_start=1 /brodutt="s-adenosy homogysteine hydrolage homolog"	
Db 972 ATT	481550 /gene="XPVkona"	CDS
QY 721 ATT	12258 '. Gene="xpvkona"	gene
Db 912 TAT	/cell_type="fibroblasts" /tissue_type="skin"	
OY 661 TAT	/organism="homo sabiens" /db_xref="taxon:9606" /chromosome="1"	
Db 852 GAT	1.	FEATURES Source
Qy 601 GAT	Submitted (19-DEC-1996) Dermatology, UCSF, 31d and Farnassus, Box 0750, San Francisco, CA 94143, USA	JOURNAL
Db 792 AAT	SION 1000 Demontal Ton 213 -3 -3 -3 -3 -3 -3 -3 -3 -3 -3 -3 -3 -3	TITLE
Оу 541 ААТ		REFERENCE
Db 732 GTT	variant by a gene on human chromosome yl homocysteine hydrolase	TOTTRUAL
Qy 481 GTT	rer, J.E. istability in the xeroder	TITLE
Db 672 AAG		AUTHORS
ОУ 421 ААС	10070969	MEDLINE
612	related to P53 function in the xeroderma pigmentosum variant Cancer Res. 59 (5), 1102-1108 (1999)	JOURNAL
Qy 361 GAT	Nagasawa, H. and Little, J.B. Increased ultraviolet sensitivity and chromosomal instability	TITLE

		AAAAATGGGCCATTCAAACCTAATTATTACAGATAC 1296	1261 1512	qq VQ
	1260 1511	TCATTTGATGCCCACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGGGACTCAAC	1201 1452	р У
	1200 1451	CAGGATGTGTACTTGCTTACCTAAGAAAATGGATGAATACGTTGCCAGCTTGCATCTGCCA	1141 1392	Dy dd
	1140 1391	GCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGCGATACAAG	1081	ρ δ
	1080 1331	GAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCATCACA	1021 1272	gy Qy
	1020 1271	GTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCTCCTGGCA	961 1212	40 40
	960 1211	CACTCCAACACAGAAATCGATGTGACCAGCCTCCGGCACTCCGGAGCTGACGTGGGAGCGA	901	DA G
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61	AGGGCAGCAGTTTCTGTGTC AGGGCAGCAGTTTCTGTGTC	y Matcl Local hes 12	VOHVYMPOKRYVILAGGELIMISTATION TO THE CONTROL OF THE	AEAGYAYEAWIGESEDFWWCIDRCYNNIDGWQANNILDGGODLTHWYXKXY NIVEKKI RGIYEESYTGYHRLYQLSKAGKLCYPAMIVNDSYTKQKEDNLYCCRESILDGLKRTTD VMEGGKQVYVGGYGEYGKGCQALKALGAIYYITEIDPICALQACMDGFRYVKLMEYT DVMEGGKQVYVGGYGEYGKGCCAALKALGAIYYITEIDPICALQACMDGFRYVKLMEYD	/PROJECTION AND 17 0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	CDS 3081810 /codon_start=1 /product="8-alenosylhomocyste! /product=14-alenosylhomocyste!	/tissue_type="Flacenta, choric /tissue_tipe="Flacenta, choric /clone_lib="NHH_MGC_21" /clone_tib="NH10B-R" /lab_host="DH10B-R" /cota="WooterDM27"	org	rints clone was selected for turn length sequencing because passed the following selection criteria: Hexamer frequency analysis, Similarity but not identity to protein. FEATURES Location/Qualifiers source 1 2526	Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 22 Row: h Column: 21	Schein, Duane Smallus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.	Sueven Jones, Jennifer Asano, Ian Bosdet, Susanna Chan, Readman Chiu, Chris Fjell, Letticia Hsiao, Martin Krzywinski, Reta K Sen Lee, Victor Ling, Carrie Mathewson, C Sen Company Professional Company	ב טוגו	Email: cgapbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Rubin Laborat	Institute USA K NIH-MGC 1	AUTHORS StrausbergyRra AUTHORS StrausbergyRra TITLE Direct Submission JOURNAL Submitted (10-MAY-2001) National Instit	NISM Homo Eukar Mamma	KEYWORDS MGC.
120 Qy	60 Qy 571 Db	9; Length 2526; Oy 0; Indels 0; Gaps 0; Db	EGRYKOD OY	Qy DD DD	Qy Db	оу рь	rcinoma" Qy	Qy da	ORF QY	d Qy	Van den Bosch, Jill Vardy, arra. Db	a Kutsche, Oliver Lee, Soo A Candice McLeavy, Steven Description De	tre, Qy	Qy Db		Qy Control Cancar Office National Cancar Office National Cancar	Qy; Vertebrata; Euteleostomi;	da
1141 CAGGATGTGTACTTGCTTACTAAGAAATGGATGATACGTTGCCAGCTTGCATCTGCCA 1200	GCCACAACAGGCTTTGGCACTGATAGAACTCTATAATGCACCGGAGGGCGATAGAAG 	1 GAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCAT¢ACA	961 GTACGTTCTCAGGTGGACCATGTCATCTGGCCAGÁTGGCAAACGAGTTGTCCTCCTĆGCA 1020 	901 CACTCCAACACAGAAATCGATGTGACCAGCCTCCGGACTCCGGAGCTGACGTGGGAĠCGA 960 	841 GTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATAT¢GGC 900 	781 AAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAAT 840	721 ATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGGATGG	661 TATGGTGAGGTAGGCAAGGGCTGCTGCTGCTCCTCAAAGCTCTTGGAGCAATTGTCTAC 720 	601 GATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGT	541 AATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTG 600	481 GTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACGTC 540	421 AAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGGAAGAGAGAG	361 GATGGGTGGCAGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACTGGGTTTAT 420 	301 GCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTGTGAACATG 360 	241 ATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGG	181 GCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGGTCAGTGCCGGTGGTCTGCTTGTAAC 240	121 GGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACACACAC	572 GAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAG 631

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This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Sequencing Group at the Stanford Human Center, Stanford University School of Medicine, Stanford, Web site:

http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (05-NOV-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Hethesda, MD 20892-2590,
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Contact: MGC help desk
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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1. .2552
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 .GTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCTCCTGGCA
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Local Similarity
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                                                                                                CACTCCAACACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCGA
                                                                                                                                                               GTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGC
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                                                          CACTCCAACACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCGA
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2563)
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HARTWDEREK NIGEL JOHN (NZ) .
Location/Qualifiers
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HVINPDGKRVVLLAECRILNISGSTVPTFVLSITATTQALALIELYNAEEGRYKQDVY
LLPKKMDEYVASLHLPSEDAHLTEITDQAKYLGLNKNGPFKPNYYRY"
604 c 677 g 636 t
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IVEESVTGVHRLYQLSKAGKLCVPAMNVNDSVTKQKFDNLYCCRESILDGLKRTTDVM
FGGKQVVVCGYGEVGKGCCAALKALGAIVYITEIDPICALQACMDGFRVVKLNEVIRQ
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the full 5' nucleotide sequence. The initiation of
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                                            GCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGCGATACAAG
                                                                                                     GAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCATCACA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Baylor College of Medicine Human Sequencing Center
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Homo sapiens, S-adenosylhomocysteine hy
MGC:8936 IMAGE:3853747, mRNA, complete
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Submitted (10-UUI-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 2583)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: villalon@bcm.tmc.edu.
villalon, D.K., Luna, R.A., Hale, S.M., Hulyk, S.,
A.M., Holloway, M., Telford, B, Hodgson, A., Bouck,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center code: BCM-HGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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RGIVEESVTGVHRLYQLSKAGKLCVPAMNVNDSVTKQKFDNLYCCRESILDGLKRTTD
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/protein_id="AAH10681.1"
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/clone_lib="NIH_MGC_65"
/lab_host="DH10B"
                                                                                /translation="matvikapkkqiqfaddmqeftkfpiktgrrslsrsisqsstds
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Lkkraqgekplagakiygcthitaqtavlietlcalgaqcrwsacniystqnevaaal
                                                                                                                                                                                                                                                                                                            /organism="Homo sapiens"
/db_xref="LocusID:107.68"
/db_xref="taxon:9606"
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                     CACTCCAACACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGGA 1530
                                                   GTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGC
                                                                                                                                                                                          AAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAAT
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_		/protein_1d="AAL26869.1" /db_xref="GI:16588687"
ОУ 781		/oroduct-"S-adenosylhomocysteine hydrolase-like protein"
Db 1383	he	and dermal denoritic cells; make increased ouring monocyte differentiation to monocyte-derived dendritic cells in the presence of GM-CSF and TL-4"
Оу 721	•	/note="DCAL; dendritic cell expressed AHCY-like protein expressed in dendritic cells in blood, Langerhans cells
Db 1323		CDS & 369. 1961
Оу 661		•
Db 1263		2011 1450 .
ду 601		/chranes 1 s
Db 1203		/organism="Homo sapiens"
Qу 541	<u> </u>	FEATURES Location/Qualifiers
Db 1143		Research Institute, Level 3, Aubigny Place, South Brisk
QУ 481		Dendritte Cell
Db 1083		AUTHORS Deker,J.W., Budhia,S., Angel,N.Z., Cooper,B.J., Clark,G.J., Hart D.N.J. and Kato.M.
ОУ 421		
Db 1023		Immunogenetics: 53; ((12), 993, 1001; (2002)
Оў 361 (TITLE Identification of an S-adenosylhomocysteine hydrolase-like transcript induced during dendritic cell differentiation
Db 963 (AUTHORS Dekker, J.W., Budhia, S., Angel, N.Z., Cooper, B.J., Clark, G.J.,
Qy 301 (Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 2677)
Db 903		Chordata. Craniata.
ОУ 241		DS .
Db 843		ON AF315687
ОУ 181 (
Db 783 (5	687 AFA15687 2677 hp mgna linear
ОУ 121		מייניים ה
Db 723 (Db 1831 AAAAATGGGCCATTCAAACCTAATTATTACAGATAC 1866
Оу 61 (QY 1261 AAAAATGGGCCATTCAAACCTAATTATTACAGATAC 1296
Db 663		1771 TCATTTGATGCCCACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGGGACTCAAC
Qy 1:		Qy 1201 TCATTTGATGCCCACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGGGACTCAAC 1260
Query Mai Best Loca Matches		QY 1141 CAGGATGTGTACTTGCTTACGTAGAAAATGGATGAATACGTTGCCAGCTTGCATCTGCCA 1200
BASE COUNT ORIGIN		QY 1081 GCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGCGATACAAG 1140
		1021 GAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCATCACA
		Db 1531 GTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCTCCTGGCA 1590
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Local Sim
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GTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGC 900
                                                 AAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAAT 840
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                         AAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAAT 1502
                                                                               GATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGGC
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LIETLCALGAÇORWSĄCNIYSTQNEVAAALAEAGVAVPAWKGESEDDWWCIDRCVNM
DGWQANMILDDGGDLTHWYKKYPNVFKKIRGIVESSYTGVHRLYQLSKAGKLCVPAM
NVNDSYTKQKEPUNYCCHEYIKLGYLKRYTDVNEGKGKYVVCGYGEYGKCCAALKALG
AIVYITEIDPICALQACMDGFRVVKLNEVIRQVDVVITCTGNKNVYTREHLDRNKNSC
TYCHNGHSNTEIDVTSLRTPELTWERVASQVDBVIWPDGKRVYLLAEGRILNLSCSTV
PIFYLGITATTQALALIELYNAPEGRYKQDVYLLPKKNDEYVASLHLPSFDAHLTELT
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648 c 708 g 664 t
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                                                                                                                                                                                                                                                                    Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone&rzpd.de Further
Information about the clone and the sequencing project is available
at http://www.mips.biochem.mpg.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                      Submitted (15-MAY-1999) MIPS, Am Klopferspitz 18a, D-82152 Martinsried, GERWANY Clone from S. Wiemann, Molecular Genome Analysis, German Cancer Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de; sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZp5664A1523) is available at the RZPD in Berlin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens mRNA;
partial cds.
AL049954
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Mammalia; Eutheria; Primates;
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                                                                                                 /map="1, 15.55 cR from D1S248"
/clone="DKFZp564A1523"
/tissuc-pe="brain"
/clone_lib="564 (synonym: hfbr2). Vector
x1-2blue; sites NotI + Sall"
/dev_stage="fetal"
/gene="DKFZp564A1523"
/note="S-adenosyl homocysteine
splice variant"
                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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 GATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGC
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TQAPSGESENLRHRQGSRAESSQNLLSIRRLYSAGGMGRSDWRMLWIQLWPELDSLE
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KQQTNSKGSSNFCVKNIKQAEFGRREIEIAEQDMSALISLRKRAQGEKPLAGAKIVGC
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CCAALKALGAIVITTELDPICALGACMGGFRVVKLNESVIRDVGKGVVVCGYGEVGKG
CCAALKALGAIVITTGALALIELYNAPEGRYKQDVYLLPKKWDEYVASLHLPS
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/product="hypothetical
/protein_id="CAB43223.;
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Submitted (03-DEC-2001) National Institutes of Health, Mammalian Submitted (03-DEC-2001) Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer Gene Collection (MGC), Cancer Genomics Office, National Cancer General MD 20892-2590,
         Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
                                                                                                   NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-rémail.nih.gov
Elssue Procurement: Gilbert Smith, Ph.D.
Tissue Procurement: Gilbert Smith, Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genom
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus (bases 1 to 1772)
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Query Match
Best Local Similarity
Matches 1215; Conserv
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, GenomeScan gene prediction, Similarity but not identification.
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LRKRAQGEKPLAGAKIVGCTHITAQTAVLIETLCALGAQCRWSACNIYSTQNEVAAAL
AEAGVAVFAWKGESEDDFWWCIDRCVNNDGWQANMILDDGGDLTHWVKKYENVFKKI
RGIVEESYTGVHRLYQLSKAGKLCVPAMNVNDSVTKQKFDNLYCCRESILOGLKRTTD
VMFGGKQVVVCGYGEVGKGCCAALKALGAIVYITEIDPICALQACMDGFRVVKLNEVI
RQUDVVITCTGNKNVTTREHLDRMKNSCIVCNMGHSNTEIDVTSLÆFPELTWERVRSQ
VDHYIMPDGKRVVLLAAEGRLLNLSCSTVPTFVLSITATTQALALIELYNAPEGRYKQD
VVLLPKKNDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGPFKPNYTRY

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/tissue_type="Mammary tumor metastatized to lung.
MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR
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/protein_id="AAH18218.1"
/db_xref="GI:17390493"
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/translation-"MATVTKAPKKQIQFADDMQEFTKFPTKTGRRSLSRSISQSSTDS
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                                                                                                                                       Homo
                                                                                         oligo capping; fis (full insert sequence). Homo sapiens colon mucosa cDNA to mRNA, clone_lib:ColF
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AK025372.1 GI:10437875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'- & 3'-end one pass sequencing: Departent of Virology and Human Genome Center, Institute of Medical Science, University of Tokyo (partly supported by Science and Technology)
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Shibahara,T., Tanaka,T. and Nakamura,Y.
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                                                                                 Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                        Homo
                                                                                                                                                                                                                                                  Homo sapiens, Similar to clone IMAGE:3536052, mRNA BC008349
BC008349.1 GI:14249935
          Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/DTP
                                                                                                                                                                                                                                                                                                            BC008349
                                         NIH-MGC Project URL: http://mgc.nci.nih.
Contact: MGC help desk
                                                                                                                                Direct Submission
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                                                                                                                                                                                          Eukaryota;
                                                                                                                                              Strausberg, R.
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Library Preparation: Rubin Laboratory
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S-adenosylhomocysteine
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1024; Conservative
GCCTGGAAGGGAGAGTCAGAAGATGACTTTTGGTGGTGTATCGATAGATGTGTGAATGTG
                                                                                                   ATCTATTCCACTCTCAATGAAGTGGCTGCTGCTCTAGCAGAAAGTGGATTTCCTGTTTTT 839
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Susanna Chan, Readman Chiu, Chris Fjell, Erin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clone distribution: MGC clone distribution
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DNA Sequencing by: Genome Sequence Centre,
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EALVSDGTVTEAPRTVKKQIOFADQKGEFNKRFKIGRSLLSKSISQSSTDSYSSAA
SYTDSSDDETSPARKQVNSKGSSDFCVKNIKQAEFGRELEIAGEMPALMALKKRA
OGEKPLAGAKIVGCTHITAQTAVLMETLGALGAQCRMAACNIYSTLNEVAAALAESGF
PYFAMKGESEDDFMWCIDRCVNVEGWOPNMILDDGGDLTHWIKX PHNFKKIKGIVE
ESYTGYHRLKQLSKAGKICYPAMNYNDSYTKOKDNLYCKRESILDGLKRTDDMKFGE
KQVVVCGYGEVGKGCCAALKAMGSIVYYTEIDPICALQACMDGFRLYKLNEVIRQVDI
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/clone_lib="NIH_MGC_7"
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Homo sapiens mRNA for KIAA0828 p
AB020635
AB020635.1 GI:4240144
 Homo
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ATCTATTCCACTCTCAATGAAGTGGCTGCTGCTCTAGCAGAAAGTGGATTTCCTGTTTT
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/protein_id="BA74851.1"
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/db_xref="G1:4240145"
/translation="EPVVAAEAVMSVQVVSAAAAAKVPEVELKDLSPSEAESQLGLST
/translation="EPVVAAEAVMSVQVVSAAAAAKVPEVELKDLSPSEAESQLGLST
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TDSYSSAASYTDSSEDDETWRCIDKOKNSKGSSDDCVKNIKQAEFGREIELAGEKNF
LMALRKRAQGEKPLAGAKIVGCTHITAQTAVLMETLGALGAQCKNAACNIYSTLNEVA
AALAESGFPVFAMKGESEDDFWRCIDKCVNVEGROPNHILDDGGDLTHWIYKKYPNKF
KKIKGIVEESYTGVHRLYQLSKAGKLCVYPAMNVNDSVTKOKFDNLYCGRESILDGLKR
TTDMMFGGKQVVVCGYGEVGKGCCAALKAMGSIVYVTEIDPICALQACMDGFRLVKLN
EVIRQYDIVITCTGNKKNVTREHLDRMKNSCIVCNMGHSKTEIDVASLKTPEELTWERV
RSQVDHVIMPDGKRIVLLAEGRILLNLSCSTVPTFVLSITATTQALALTELINAPEGRY
KQDVYLLEKKMDSTVASSHLPTEDAHLTELTDEQAKYLGLNKNGFFKPNYYRY"
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/clone_lib="pBluescriptII
/dev_stage="adult"
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/db_xref="taxon:9606"
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GAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCTÇAG
                                                                     TCTAAGGGAAGCAGTGACTTCTGTGTTAAGAACATCAAACAGGCAGAGTTTGGACGAAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.g. Series: IRAK Plate: 22 Row: 1 Column: 22 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (01-MAR-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11AO3, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dickson, M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Web site:
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KKMDEYVASLHLPTFDAHLTELTDEQAKYLGLNKNGPFKPNYYRY"
1 1184 c 1145 g 1423 t
                                                                                                                                                                                                                                                                                            ESVTGVHRLYQLSKAGKLCVPAMNVNDSYTKQKFDNLYCCRESILDGLKRTTDMMFGG
KQVVVCGYGEVGKGCCAALKAMGSIVYVTEIDPICALQACMDGFRLYKLNEVIRQVDI
VITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVASLRTPELTWERVRSQVDHVI
                                                                                                                                                                                                                                                                                                                                                      SYTDSSDDETSPRDKQQKNSKGSSDFCVKNIKQAEFGRREIEIAEQEMPALMALRKRA
QGEKPLAGAKIVGCTHITAQTAVLMETLGALGAQCRWAACNIYSTLNEVAAALAESGF
PVFAWKGESEDDFWWCIDRCVNVEGWQPNMILDDGGDLTHWIYKKYPNMFKKIKGIVE
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EALVSPDGTYTEAPRTVKKQ1QFADQKQEFNKRPTK1GRRSLSRSISQSSTDSYSSAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo_sapiens"
/db_xref="LocusID:23382"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /protein_id="AAH24325.
/db_xref="GI:19353092"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="KIAA0828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Uterus, leiomyosarcoma"
/clone_lib="NIH_MGC_71"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="MGC:21525 IMAGE:3907552"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                            translation="MSVQVVSAAAAAKVPEVELKDLSPSEAESQLGLSTAAVGAMAPP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note="Vector: pCMV-SPORT6"
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                                                                                                                         Score 861.4; DB 9;
Pred. No. 1.4e-257;
0; Mismatches 271;
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1200	1141 CAGGATGTGTACTTGCTTACGAAGAAAATGGATGAATACGTTGCCAGCTTGCATCTGCCA	Q
PAAG	1081 GCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCGAGGGGGGATAC 	B 5
ACT	021 GAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCATC	B 8
GCA CA CA	961 GTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCTCCTGG 	g 2
∯ – ĝ	901 CACTCCAACACAGAAATCGATGTGACCAGCCTCCGGACTCCGGAGCTGACGTGGGAGC 	B 8
≱ _ ຕ	841 GTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGG 	β 6
H-H	781 AAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAA 	용 <i>성</i>
ଦ ≯	721 ATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATGGATGG	용 성.
н C	661 TATGGTGAGGTAGGCAAGGGCTGCTGTGCTGCTCTAAAGCTCTTGGAGCAATTGTCTAC 	B 성
$\alpha - \alpha$	601 GATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGT	β &
- 4	541 AATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTG	B 8
(3-(3	481 GTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACGTC	D 04
ي- حر	421 AAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGAAGAGAGGGGTGACTGGT	D Oy
	361 GATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACTGGGTTTAT	D S
41 — 41	301 GCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTGTGAACATG 	B &
(1	241 ATCTACTCAACTCAGAATGAAGTAGCTĞCAGCACTGGCTGGAGGCTGGAGTTGCAGTGTTC	g Qy
0-0	181 GCGGTGTTGAGTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTGTAAC	р _О
H Þ	121 GGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACACACATCACAGCCCAGAC	D Qy
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TGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTGCTCCTCAAAGCTCTTTGGAGCAA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAAAATGGGCCATTCAAACCTAATTATTACAGATA 1295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yu,W., Sarginson,J. and Gibbs,R.A. Direct Submission
Submitted (20-NOV-1997) Molecular and College of Medicine, One Baylor Plaza Location/Qualifiers
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AF035319
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Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., L
Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A.
Large-scale concatenation cDNA sequencing
Genome Res. 7 (4), 353-358 (1997)
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97264341
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                                                                                                                                                           370
                                                                                                                                                                                                                                                                                                                                                 /tissue_type="brain"
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/dev_stage="infant"
/dev_stage="infant"
/note="This clone is similar to
encoded by GenBank Accession Nu
Consortium clone ID number is 2
                                                                                                                                                           ø
                                                                                                                                                                                        /protein_id="Aab88189.1"
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/trans1ation="prancygevgkgccaalkalgalvyiteidpicaloacmdgfr
/trans1ation="prancygevgkgccaalkalgalvyiteidpicaloacmdgfr
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PEGRYKQDVYLLPKKMDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGPFKPNYYRY
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                  note-"similar to S-adenosylhomocysteine hydrolase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                              sex="female
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S930, Houston, TX 77030,
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This clone was sequenced as part of a high-throughput process to sequence clones from Drosophila Gene Collection 1 (Rubin et al., Science 2000). The sequence has been subjected to integrity checks for sequence accuracy, presence of a polya tail and contiguity within 100 kb in the genome. Thus we believe the sequence to
                                                                                              Berkeley, CA 94720, USA
Sequence submitted by:
Berkeley Drosophila Genome
Lawrence Berkeley National
                                                                                                                                                                                 Direct Submission Submitted (16-MAY-2002) Berkeley Drosophila Genome Project,
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priming, priming from contaminating genomic DNA, retained introns due to reverse transcription of unspliced precursor RNAs, and reverse transcriptase errors that result in single base changes. For further information about this sequence, including its location and relationship to other sequences, please visit our Web site
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1323)
                                                                                                              Homo sapiens, Similar to clone IMAGE: 3010755, mRNI
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599; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (26-FEB-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             contact: amadan@systemsbiology.org
Anup Madan; Rachel Dickhoff, Jessica Fahey,
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Contact: MGC help des
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CTGNKRYVTREHLDRЖKNSCIYCNMGHSNTEIDVTSLÆFÞELFWERVEĞQVDHYIMPD
GKRVVLLAEGRLLNLSCSTVPTFVLSITATTQALALIELYNAÞEGRYKQDVYLLÞKKM
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ACC 549	Db 490 ACGITGCCAGCTTGCATCTGCCATCATTTGATGCCCACCTTACAGAGCTGACAGATGACC
ACC 12:	QY 1178 ACGTTGCCAGCTTGCATCTGCCATCATTTGATGCCCACCTTACAGAGCTGACAGATGACC 1237
AT 48	Db 430 ATGCACCCGAGGGGCGATACAAGCAGGATGTGTACTTGCTTACGAAAAATGGATGAAT 489
AT 11:	QY 1118 ATGCACCCGAGGGGGCGATACAAGCAGGATGTGTACTTGCTTACCTAAGAAAATGGATGAAT
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	U	o vo				:	nzyme; S-a activity; e disease;	sequence	(fir		standard				•									18.6								
	96NZ-0299507 N J.				Location/G 31847 /*tag= a /product=			0f	rst entry)		d; cDNA;		1396 1396	1941	929	. 58909	1812	349980 1812	1939	1557	1494	1728	4411529	1461	1727	939	2211	435 384	1592	2658	636	504 5537
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					/Qualifiers a - "DD4b5.3 enzyme"		enosyl-L-homocysteine hydrolass stimulation; inhibition; dendri transplantation; ss.	ODD4b5.3 enzyme.			3 BP.	ALIGNMENTS	AAF71864 AAS95123	AAT44515	AAF14585	AAT44513 AAF28543	AAQ29419	AAH68526 AAT29194	ABK52394	AAF71862	AAC46817	AAC39836	AAI99682	ABN/3/04 AAS09278	AAC46315	AAS76217	AAC91228	ABV14215 ABN93848	ABL28157	ABV23126	AAZ80766	ABV44141 ART.29786
	·						se-type activity; ritic cell; cancer;						Corynebacterium gl	Arabidopsis S-aden	Aspergillus oryzae	ment	Nicotiana tabacum	C glutamicum codin	SahH gene encoding	Corynebacterium gl	Arabidopsis thalia	Arabidopsis thalia	Mycobacterium tube	Trichomonas vagina	Arabidopsis thalia	DNA encoding novel	Human S-adenosylho	Human prostate exp Gene #346 used to	Drosophila melanog	Human cancer assoc Human prostate exp	colon cance	prostate ex phila melano

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Matches 1296; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New isolated S-adenosyl-L-homocysteine hydrolase enzyme - i develop products which can be used in the treatment of e.g. auto-immune disease, transplantations or cancers
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DB; AAW56097.
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                                             GTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGGCCATGAACGTC
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nilarity 100.0%;
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16-MAR-2000;
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      Schlegel
                                   18-JUL-2000;
13-DEC-2000;
                                                                                       20-FEB-2001;
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                                  2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-219007P.
2000US-255281P.
                                                                                       2001WO-US05171
                                                                                                                                                                                     (first entry)
       Endege WO,
                                                                                                                                                                      expression marker cDNA
                                                                                                                                                cancer; cytostatic; carcinogen;
marker; gene; ss.
                    PREDICTIVE
       Monahan
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2001-662795/76

Claim

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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) assessing whether a patient is afflicted with prostate cancer; (b) monitoring the progression of prostate cancer in a patient; (c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient (f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastazed in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                               GAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAG
 GATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGGAGACTTAACCCACTGGGTTTAT
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                                                                                                                                                                                                                                                  Human; prostate pharmacogenomic
                                                                                                                                                                                                                                                                                                                                                                    ABV29032;
                                                                                                                                                                                                                                                                                                                                                                                                       ABV29032 standard; cDNA; 3634
                                                                                  17-FEB-2000;
                                                                                                                                                                                 WO200160860-A2
                                                                                                                                                                                                                                                                                                                                       16-SEP-2002
                                                                                                                   20-FEB-2001;
                                                                                                                                                    23-AUG-2001
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2000US-183319P.
2000US-189862P.
2000US-207454P.
2000US-211314P.
2000US-211314P.
2000US-255281P.
                                                                                                                   2001WO-US05171
                                                                                                                                                                                                                                                    cancer;
                                                                                                                                                                                                                                                                                                    expression marker cDNA 29023
                                                                                                                                                                                                                                                  cytostatic;
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The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 1; Page 6147-6148; 11750pp; English.

    (e) selecting a composition for inhibiting prostate cancer in a patien
    (f) assessing the prostate cell carcinogenic potential of a compound;
    (g) determining whether prostate cancer has metastasized in a patient;
    (h) assessing the aggressiveness or indolence of prostate cancer in a

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (d) assessing the
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                                            GATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACTGGGTTTAT
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                                                                                                              GAT@GGTGGCAGGCCAACATGATCCTGGATGATGGGGGGAGACTTAACCCACTGGGTTTAT
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             AATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTG
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US5854023-A.
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                             "SAHH"
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CC The SAHH protein can be used to generate specific antibodies and in drug CC screening to identify specific binding agents. Antagonists of the protein are used to treat or prevent a wide range of viral, bacterial, CC fungal, parasitic, protozoal or helminthic infections, many cancers (leukaemia, lymphoma or solid tumours), and many autoimmune diseases (e.g. acquired immune deficiency syndrome, allergy, asthma, diabetes cellitus, multiple sclerosis etc). All these conditions may be treated by expressing antisense sequences, triplex-forming agents or ribozymes CC directed against the nucleic acid. The nucleic acid and its fragments can be used as probes or primers for detecting and quantifying gene capression, for diagnosis or monitoring of disease, to identify genetic variations, mutations or polymorphisms, in gene mapping and as antisense therapeutics. Antibodies are used directly as antagonists, indirectly to deliver active agents to SaHH-expressing cells, to diagnose and monitor CC diseases in standard immunoassays, in competitive drug screens and to isolate the protein from natural sources.
                                                                                                                                                                                                                                                                                                                                                                                           Best Local Sim
Matches 1295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acid encoding human S-adenosyl-5-homocysteine hydrolase for production of recombinant enzyme, useful for diagnosis, treatment and prevention of cancers, infections and autoimmune
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Human; chromosome mapping; gene mapping; gene therapy; food supplement; medical imaging; diagnostic; genetic (

disorder; forensic;

88

novel human diagnostic protein #12020

DNA encoding

Homo sapiens. W0200175067-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 62.9%;
Best Local Similarity 78.8%;
Matches 1023; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-639362/73.
P-PSDB; ABG12029.
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23-AUG-2000; 2000US-0649167.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and to produce other types of data and products dependent on DNA and main acid sequences. AAS64197-AAS94564 represent novel human diagnostic coding sequences of the invention of appear in the printed Note: The sequence data for this patent did not appear in the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID No 12020; 103pp; English
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ATCTATTCCACTCTCAATGAAGTGGCTGCTGCTCTAGCAGAAAGTGGATTTCCTGTTTTT 4170
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RESULT 6
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ABL03693 standard; cDNA; 1566

CTTGCACAGGAAAI	TITEGETANCEAGANATCACTANATTACTACAGATA 12: 1	Db 368 Qy 84 Qy 90 Qy 90 Qy 95 Qy 95 Qy 101 Qy 107 Qy 107 Qy 107 Qy 113 Qy 113 Qy 115 Qy 115 Qy 115 Qy 125
CTTGCACAGGAAATAAGAA 839	TETTGETAACCAGAGAGCCTTAGACCGTATGAGATTAG CCACTCCAACACAGAAATCGATTGACCGTATGAGACTTCGAGCTCCGCAC	
CTTGCACAGGAATAAGAA 839 CTTGTACAGGAATAAGAA 363 GTATCGTATGCAATATGG 899 [TITGGTAACCAGAAATGAATGAACGTTATGAACAGAATAGA CCACTCCAACACAGAAATGAATTGACGTGGCGACCAGCAGAATAGACCATTGACCAGCAGTCCGGAC	36 8 8 35 9 36 8 8 32 11 33 10 34 00 35 9 36 8 32 11 33 33 33 34 00 35 35 35 35 35 35 35 35 35 35 35 35 35
CTTGCACAGGAAATAAGAA 839	9 TETGETAACCAGAAATGAATTGAACCGTATGAAGAATTAG CCACTCCAACACAGAAATGAATTGAACCGTATGAAGAATTAG CCACTCCAACACAGAAATTGAACTGACCGTATGAAGAATTAG CCACTCCAACACAGAGATTGACGTGGCGAGTCTGCGGAC 9 GAGTACGTTCTCAAGTGACCATGTCATCTGGCCAGATTG	36 8 35 35 36 36 36 36 36 37 37 31 31 31 31 31 31 31 31 31 31 31 31 31
CTTGCACAGGAAATAAGAA 839	TITIGETAACCAGAAGAGCCTTGGAGCAGTTGAGCTCAAGAATAG CCACTCCAACACAGAAATGGATGTGACCAGCTCCGCAC	36 8 35 35 35 31 31 31 31
CTTGCACAGGAAATAAGAA 839	TGTGGTAACCAGAGAGCTTGGACCGTATGAAGAATAG CCACTCCAACACAGAAATCGATTGGACCGTATGAAGAATAG CCACTCCAACACAGAAATCGATTGGACCAGCCTCCGCAC	1 3 1 3 5 5 6 8 6 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1 3 1
CTTGCACAGGAAATAAGAA 839	9 TETTGETAACCAGAAGAGCACTTGGACCGTATGAAGAATAG CCACTCCAACACAGAAATCGATTGGACCAGCAGCTCCGCAC	36 35 35 35 36 36 36
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-	1 AAGCTAAATGAAGTCATCCGGCAAG-TCGATGTCG	0у 78
PATGGATGGATTTCGACTGG	9 GTAACTGAAATTGACCCCATCTGTGCCCTGCAAGCCTG	Db 374
CATGGATGGGTTCA	1 ATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTG	0у 72
ATTGTGT) TATGGAGAGGTGGGAAAGGGTGCTGTGCTGCCGCTGAAAGCCATGGGCTCC	Db 380
ATTGTC	1 TATGGTGAGGTAGGCAAGGGCTGCTG	Ωу 66
CAAGTGGTAGTCTGTGG	59 GATGGACTTAAAAGGACAACAGACATGATGTTTGGTGGAAAG	Db 386
AAGTGGTGGTGTGTG	1 GATGGCCTGAAGAGGACCACAGATGTGATGTTTG	Ωу 60
CIGITGCCGIGAATCAATICIT 3870	9 AATGACTCAGTCACCAAACAGAAATTTGACAACCTCTACT	Db 392
GCTGCCGAGAATCCATT	1 AATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACT	Оу 54
GTTCCAG	GTTCACAGGCTGTACCAACTGTCCAAAGCTGGGAAGCTGTG	Db 398
TETTCCGGCCATGAACGT	TOTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTG	ΩУ 48
TAGAGGAGAGTGTTACTG	9 AAAAAGTATCCCAACATGTTTAAGAAAATCAAGGGCA	Db 404
STGGAAGAGAGCGTC	1 AAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCA	Оу 42
ACTTAACCC	9 GAGGGCTGGCAGCCAACATGATCCTGGATGATGAGGGGAGGGGAGCCAACATGATCTTGGATGATGATGAGGGGGGGG	Оу 36 Db 410
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Best Local :
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                                                                                                                                                                                                                                                                                       The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                              New isolated nucleic acid genes from Drosophila and interactions -
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P-PSDB; ABB59590.
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New isolated nucleic acid genes from Drosophila and interactions
                                                                                                                                                                                                                                                                                                                                                                                                 The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-MAR-2000;
11-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                             Sequence 1776 BP; 437 A; 432 C; 479 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID NO 40834;
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Pred. No. 9.7e-194;
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                                                                         29-MAY-2001; 2001WO-US17756
                                                                                                                                  06-DEC-2001.
                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                             Human; ovarian
                                                                                                                                                                                                                                                                                                                                                      Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1272 GGCTGGTCAATCTGAGCTGCTCCAGCATCCCCTCGTTCGCCGTGTCTATCACCTCGGCCA
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                      26-MAY-2000; 2000US-207484P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AGGCAAGGGCTGCTGTGCTGCTCA---
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                                                                                                                                                                                                                                                                                                                                                   ovarian
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                                                                                                                                                                                                                                                                                                                                                   cancer related
                                                                                                                                                                                                                                                                                             cancer; ovarian tumour; cytostatic; gene;
                                                                                                                                                                                                                                                                                                                                                   cDNA clone SEQ ID NO: 2023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
les 510; Conserv
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                                                                                                                                                                         CATGACACCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGCG
                                                                                                                                                                                                                                                   CCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCCACCTTTGTTCTGTC
                                                                                                                                                                                                                                                                                                                            GGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                        TATGGGCCACTCCAACACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAA 893
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TATGGGCCACTCCAACACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTG
                                                                                                               ATACAAGCAGGATGTGCTTGCTTCCTAAGAAAA-TGGATGAATACGTTGCCAGCTTGC
                                                                                                                                                                                                                                                                                                        GGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGAT-GNAAACGAGTTGTCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAA
 ATCTGCCATCATTTGNTGCCCACCTTACAGAGCTGACAGATGNCCAAGC-AAATATCTGG
                                   ATCTGCCATCATTTGATGCCCACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGG
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97.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 461.4; DB 24; Length 553;
Pred. No. 1.4e-139;
0; Mismatches 9; Indels 5;
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RESULT 10
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Best Local
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                         a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (1) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                Novel isolated nucleic acid molecule associated with cancerous state prostate cells and correlating with presence of prostate cancer, use for detecting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; prostate cancer; cytostatic; carcinogen;
pharmacogenomic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1253
                                                                                                                                       Sequence
                                                                                                                                                                               patient;
                                                                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid molecule (I) domprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 8770; 11750pp; English.
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                                                                                                                                                                                                                                                 in a patient;
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                                                                                                                                                                                                                                                              (d) assessing
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 218
                                                                                                                                                                                         selecting a composition for inhibiting assessing the prostate cell carcinogeni determining whether prostate cancer has assessing the aggressiveness or indolen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GACTCAACAAAATGGGCCATTCAAACCTAATTATTACAGATAC
                                           GTACACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGGCTC
AGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG
                            GTACACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCCTGGGGGCCTC
                                                                                                                                                                also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                              Similarity
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                                                                                                                                        504
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; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
; 2000US-219007P.
                                                                                   Conservative
                                                                                                                                        BP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expression marker cDNA
                                                                                                                                        117
                                                                                                                                                                                                                                                              efficacy of a therapy for inhibiting prostate cancer
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                                                                                             32.6%;
                                                                                                                                     A; 150
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                                                                                           Score 422; DB 23; Pred. No. 9.2e-127;
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                 useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB7737-ABB72072).

The segmence (ABC0737-ABB72072).
                                                                                                                           New isolated nucleic acid genes from Drosophila and
                                                                                                   Claim 1; SEQ
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11-JUL-2000;
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2000US-0614150.
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                                                                                                    ID NO 40831;
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       for this patent did not form part of the printed twas obtained in electronic format directly from
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GAAACAAAAATGTTATTACCAGGGATCACATGAATCGCATGAAGAATGGTTGTATCCTCT
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                                                                                    TCCGGGTGGTACGGCTCAACGAGGTCATCAGGACGGTGGATGTGGTGGTTACGGCAACTG
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                   AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The cDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The cDNA clones can be used for developing agents for the diagnosis and treatment of
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disorders
dysplasia
                                                                                                                                             Novel nucleic acids, used to develop products for the diagnosis treatment of disorders involving unwanted cell proliferation, particularly cancers, especially colon cancer
                                                                                                                                                                                                                            Endege WO,
Carroll E,
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                                                                                                                    Claim 15 Page 469; 469pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                   gene expression product; diagnosis; tumour; colon cancer
ctal adenocarcinoma; cell line SW480; cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard; cDNA; 636
involving unwanted or hyperplasia
                                                                                                                                                                                                                            Catino
                                                                                                                                                                                                                            Steinmann
Catino TJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      cancer cell line
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                                                                                                                                                                                                                                                                                                       99WO-IB01062
                                                                                                                                                                                                                          KE, Astle JH,
, Derti A, Fo
            cell proliferation, such as neoplasia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SW480 cDNA clone SEQ
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                                                                                                                                                                                                                            JH, Burgess CC,
Ford DM, Lewis
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                                                                                                                                                                                                                                      Bushnell SE;
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Matches.
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                                                                                                                                                                                                                                                                                                                   Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatic; proliferative; vulnerary; immunomodulator; antificiabetic; antiasthmatic; antinheumatic; antiarthritic; antiviral; antiinflammatory; antihyroid; antialtergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoletic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
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WPI; 2000-587533/55
P-PSDB; AAB43614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAC77823 standard; cDNA; 2200
                                                   Rosen CA,
                                                                                                                                12-MAR-1999;
                                                                                                                                                                    08-MAR-2000;
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                                                                                           (HUMA-) HUMAN GENOME
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                                                                                                                                                                                                                                                                                 sapiens
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418; Conserv
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                                                     Ruben SM,
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                                                                                                                                                                    2000WO-US05882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   associated gene sequence
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Pred. No. 1.3e-121;
0; Mismatches 1;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAC77607 to AAC78448 encode the human cancer associated proteins given in AAB43398 to AAB44239. The proteins can have activities based on the tissues and cells the genes are expressed in Example of activities include: cytostatic; proliferative; vulnerary; immunomodulator; antidibetic; antiathmatic; antiatheriari; antinflammatory; antityroid; antiatherial; antiathartarial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antiportiate; and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating of ameliorating medical conditions and diagnosing pathological conditions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2200 BP; 546 A; 578
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ACCTCTATGGCTGCCGGGAGTCCCTCATAGATGGCATCAAGCGGGCCACAGATGTGATGA
                   ACTIGTACTGCTGCCGAGAATCCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGT 631
                                                                                                                          GGAAGCTCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATA
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Pred. No. 5.7e-120;
0; Mismatches 521;
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17-FEB-2000;
16-MAR-2000;
                                                20-FEB-2001;
                                                                                                                   WO200160860-A2
                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                  Human; prostate pharmacogenomic
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 2000US-183319P
2000US-189862P
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                                                                                                                                                                                  cancer; cytostatic; carcinogen; pharmacodyanamic marker; gene; ss.
                                                                                                                                                                                                                                                                                                                                      cDNA; 2658
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Query Match 31.0
Best Local Similarity 58.4
Matches 741; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule (I) com a nucleotide sequence given in Tables 1-9 (ABY00010-ABY62213) of t specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-662795/76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (d) assessing the efficacy of a therapy for
in a patient;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cancer in a patient;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastatzed in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGGAGATTGCAGAGCAAGACATGTCTG 91
                                                                                                                                                               TGTGGTGCATTGAGCAGACCCTGTACTTCAAGGACGGCCCCCTCAACATGATTCTGGACG
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GGAAGCTCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATA 571
                                               GAGGCATCTCTGAGGAGACCACGACTGGGGTCCACAACCTCTACAAGATGATGGCCAATG
                                                                          GAGGCATTGTGGAAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTG
                                                                                                                            ATGGGGGAGACTTAACCCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCC
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                                                                                                         ACGGGGGCGACCTCACCAACCTCATCCACACCAAGTACCCGCAGCTTCTGCCAGGCATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            also useful as a pharmacodyanamic or pharmacogenomic marker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 4141-4142; 11750pp; English.
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; 2000US-211314P.
; 2000US-219007P.
; 2000US-255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 402.4; DB 23;
Pred. No. 6.4e-120;
0; Mismatches 521;
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   23-AUG-2001
                                                                                         Human; prostate pharmacogenomic
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                                                             Homo sapiens
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                                                                                                                                                   (first entry)
cancer; cytostatic; carcinogen;
marker; gene; ss.
                                                                                                                                                                                                                                                                                cDNA;
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                                                                                              CDNA 28958
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Best Local Similarity
Matches 741; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 6122; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI;
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09-JUN-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               selecting a composition for inhibiting prostate cancer in a patient; assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient; assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                        CATTGCCAAGGCTGGCATTCCGGTGTATGCCTGGAAGGGCGAAACGGACGAGGACTACC
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 GAGGCATTGTGGAAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTG
                                                  ATGGGGAGACTTAACCCACTGGGTTTATAAGAAGTTATCCAAACGTGTTTAAGAAGATCC
                                                                                                                              GGTGGTGTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATG
                                                                                                                                                                                          CACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCT
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                              ACGGGGGCGACCTCACCAACCTCATCCACCAAGTACCCGCAGCTTCTGCCAGGCATCC
                                                                                               TGTGGTGCATTGAGCAGACCCTGTACTTCAAGGACGGCCCCTCAACATGATTCTGGACG
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2000US-207454P.
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Pred. No. 6.4e-120;
0; Mismatches 521;
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                                                                                                                                                                                                                                                                                                                                                          CAGATGGCAAACGAGTTGTCCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCA 1051
                                                               CTGAGAAGCCAAGCCCAGTACCTGGGCATGTCCTGTGATGGCCCCTTCAAGCCGGATCACT
                                                                                               CAGATGACCAAGCAAAATATCTGGGACTCAACAAAAATGGGCCCATTCAAACCTAATTATT
                                                                                                                                 TGGATGAGGCAGTGGCTGAAGCCCACCTGGGCAAGCTGAATGTGAAGTTGACCAAGCTAA
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                              ACAGATAC 1296
                                                                                                                                                                  TGGATGAATACGTTGCCAGCTTGCATCTGCCATCATTTGATGCCCACCTTACAGAGCTGA
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/BCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-08-896-005-2
US-09-347-878-3
US-09-081-157A-8
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US-09-081-395-8
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US-09-081-395-6
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OTHER INFORMATION: n - A

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APPLICANT: Monahan, John E.
APPLICANT: Monahan, John E.
APPLICANT: Schlegel, Robert
TITLE OF INVENTION: NOVEL HUMAN GENES AND G:
TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/328,111
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: US 60/088,801
EARLIER FILING DATE: 1998-06-10
NUMBER OF SEQ ID NOS: 850
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Best Local Similarity
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APPLICANT: Steinmann, Kathleen
APPLICANT: Astle, Jon H.
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  CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGT
                                                                                      AGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG
                                                                                                                       AGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG
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US-08-191-706-4
US-09-153-751-4
US-09-381-862-6
US-09-381-862-6
US-09-770-170-7
US-09-522-211-7
US-09-040-005-1
US-08-162-809-11
US-08-162-809-11
US-09-461-697-414
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CURRENT APPLICATION NUMBER: US/09/318,448
CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 2211
TYPE: DNA
ORGANISM: Homo sapiens
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APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING,
TITLE OF INVENTION: DEVELOPMENTAL DISORDERS
FILE REFERENCE: 601-1-057
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                                                                                                                          GGTGGTGTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATG
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                                            ACGGGGGCGACCTCACCAACCTCATCCACACCAAGTACCCGCAGCTTCTGCCAGGCATCC
                                                                         ATGGGGGAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCC
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Pred. No. 1.6e-90;
0; Mismatches 306;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: Human S-adenosylhomocysteine PUBLICATION INFORMATION: DATABASE ACCESSION NUMBER: M61831/GenBank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/347,878C CURRENT FILING DATE: 1999-07-06 NUMBER OF SEQ ID NOS: 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yuan, Chong
TITLE OF INVENTION: METHODS AND COMPOSITIONS
FILE REFERENCE: 25885-1651
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                                                                      GGGCTCAGTGCCGCTGGTCTGCTAACATCTAACTCAACTCAGAATGAAGTAGCTGCAG
                                                                                                                CTGGCTGCCTGCACATGACCGTGGAGACGGCCGTCCTCATTGAGACCCTCGTCACCCTGG
                                                                                                                                           CTCTGATTTCACTCAGGGAAACGTGCTCAGGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAG 151
                                                                                                                                                                                                                                 ACATCGGCCTGGCTGCCTGGGGACGCAAGGCCCTGGACATTGCTGAGAACGAGATGCCGG 138
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                                                       GTGCTGAGGTGCAGTGGTCCAGCTGCAACATCTTCTCCACCCAGAACCATGCGGCGGCTG
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Pred. No. 1.6e-90
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APPLICANT: FRASER, CLAIRE M.

APPLICANT: VENTER, JOAN C.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SEQ ID NO 1
SEQ ID NO 1
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; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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US-09-103-840A-1/c
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                                                                                               DD 3629036 ACAAGTGGACCAAGATAGCCGAGTCGGTCAAGGGCGTCACCGAGGAGACCACCACCACCGCG 3628977
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Best Local Similarity
Matches 499; Conserv
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                                   3628976 TGCTGCGGCTCTACCAATTCGCCGCGGCCGGGGATCTGCCCTTCCCGGCGATCAACGTCA 3628917
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TYPE: DNA
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                                                     TTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACGTCA 541
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                                                                                                                                                               Conservative
                                                                                                                                                                              18.2%;
                                                                                                                                                             Score 236.2; DB 4;
Pred. No. 1.4e-63;
0; Mismatches 373;
                                                                                                                                                                                             Length 4411529;
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                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application Patent No. 5910444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3628376 ACAGCTTCGCTAACCAGACGATCGCCCAGATCGAGCTGTGGACCAAGAACGACGACGAC---T 3628320
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                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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                                                                                                                                                                                                          APPLICANT: TANAKA, E
APPLICANT: KUWATA, S
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1256 TCAACAAAAATGGGCCATTCAAACCTAATTATTACAGATAC 1296
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  COMPUTER READABLE MEDIUM TYPE: FI
                                                                                                                                                              NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           602 ATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGGTGTTGTGGCT
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                                                               COUNTRY:
                                                                                                      CITY: FALLS CHURCH
                                                                                                                           STREET:
                                                                                                                                             ADDRESSEE:
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                                                                                                                           E: BIRCH, STEWART, KOLASCH AND BIRCH
PO BOX 747
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UEHARA, KYOKO
                                                                 USA
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Floppy disk
                       FORM:
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ORGANISMS IN WHICH THE EXPRESSION
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; MOLECULE TYPE: cDNA to mRNA
JS-08-669-536-1
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Best Local Similarity 56.4
Matches 499; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
1075 ATCACAGCCACAACAGAGCTTTTGGCACTGATAGAACTCTATAATGCACC---CGAGGGG
                                                                                                                         1018
                                                                                                                                                                                                                                                  1114 TTTGACAACGAAATCGACATGCTTGGTCTCGAGACCTACCCTGGTGTCAAGAGGGATCACA 1173
                                                                                                                                                                                                                                                                                                                                                   1054 ATCATGGTTGACCACATGAGGAAGATGAAGAACAATGCCATTGTTTGCAACATTGGTCAC
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NAME: MURPHY JR, GERALD M
REGISTRATION NUMBER: 28,977
REFERENCE/DOCKET NUMBER: 1254-128
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOETWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                     904 TCCAACACAGAAATCGATGTGACCAGCCTCCGCAC---TCCGGAGCTGACGTGGGAGCGA
                                                                                                                                                                                                           961 GTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAG---TTGTCCTCCTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                634 AAATATACCAAGATGAAGGAAAGACTCGTCGGTGTTTCTGAGGAAACTACCACTGGAGTT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 AAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGAAGAGAGCGTGACTGGTGTT 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
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                                                                      GCTGAGGGTCGTCTCATGAACTTGGGATGTGCCACAGGACACCCTAGTTTTGTGATGTCG
                                                                                                                  GCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACC---TTTGTTCTGTCC
                                                                                                                                                                                                                                                                                                                                                                              GTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATGTA 843
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                                                                                                                                                                     ATTAAGCCTCAAACCGACAGATGGGTCTTCCCTGACACCAACAGTGGCATCATTGTCTTG
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                                                                                                                                      ; NAME/KEY: CDS; LOCATION: 26..148; COTHER INFORMATION: US-08-930-894-1
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US-08-930-894-1
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                                                                                   Query Match
Best Local
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GENERAL INFORMATION:
                                                                     Matches
                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE: ORGANISM: SHH GENE FROM A
                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9
FILING DATE: 10-APR-1995
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
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                424 AAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGAAGAGAGCGTGACTGGTGTT 483
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596 AAGTACAGGAAGATGAAGGATAGGATTGTCGGTGTGTCGGAGGAGACCACCACCGGGGGTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: PCT/
FILING DATE: 10-APR-1996
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TOPOLOGY: lin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/930,894 FILING DATE: 09-OCT-1997
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OPERATING SYSTEM:
MS Word
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ICANT: SKIPSEY, Marc
ICANT: WARNER, Simon
E OF INVENTION: S-ADENOSYL-L-HOMOCYSTEIN HYDROLASE PROMOT
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1100 New York Avenue, N.W.
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                                                                     Conservative
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                              APPLICANT:
APPLICANT:
APPLICANT:
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                                                                       CORRESPONDENCE ADDRESS:
                                                                                         TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEINE HYDROLASE NUMBER OF SEQUENCES: 5
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                                                     DDRESSEE:
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                 Palo Alto
 CA
                                                                                                                            Corley, Neil C.
Lal, Preeti
Shah, Purvi
                                   3174 Porter Drive
                                                                                                                                                                                    Hillman,
                                                     Incyte Pharmaceuticals,
                                                                                                                                                                                      Jennifer L
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RESULT 8
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APPLICANT: Yuan, Chong
                                                                                                                                                                                                                                          SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2226
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application Patent No. 6376210
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                                                                                                                                                                                                                                                                                                   FILE REFERENCE: 25885-1651
CURRENT APPLICATION NUMBER: US/09/347,878C
CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
            OTHER INFORMATION: Polynucleotide encoding human OTHER INFORMATION: S-adenosyl-5-homocysteine hydrother information: from bladder; n-a, c, g, or t PUBLICATION INFORMATION: PATENT DOCUMENT NUMBER: 08/896,005
PATENT FILING DATE: 1997-07-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 415-845-4166 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES
PUBLICATION DATE: 1998-12-29
                                                                                                                                     NAME/KEY: misc_feature LOCATION: (1)..(2226)
                                                                                                                                                                                 ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/8 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
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LENGTH: 2226 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Billings, Lucy J
REGISTRATION NUMBER: 30
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Pred. No. 3e-27;
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9.0%;

Score 117;

DB 4;

Length 2226;

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                                                                                                                                                                                                        Matches 126;
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APPLICATION NUMBER: US/08/204,740
FILING DATE: 04-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPUTER:
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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NAME: NO. 5753432nan, Kevin
REGISTRATION NUMBER: 35,303
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                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: cDNA
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195 CTGGCTGCCTGCACATGACCGTGGAGACGGCCGTCCTCATTGAGACCCTCGTCACCCTGG
                                                                135 GCCTGATGCGTATGCGGGAGCGGTACTCGGCCTCCAAGCCACTGAAGGGCGCCCCGCATCG 194
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                             CITY: Chicago
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                                                                                                                                                                                                                            Match 5.6%;
Local Similarity 58.6%;
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10 S. Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                                                                                                                                                                                             312-715-1234
                                                                                                                                                                                                                                                                                                                                                                    289 base pairs
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Pred. No. 1.6e-13;
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Genes Associated with Malignant
                                                                                                                                                                                                                                              Length 289;
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Best Local Similarity 58.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/081,167A
FILING DATE: 18-MAY-1998
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NAME: NO. 6083745nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,35
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MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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                                     212 GGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTAC 246
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255 GIGCIGAGGIGCAGIGGICCAGCIGCAACAICIIC 289
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STATE: Illinois
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ZIP: 60606
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                                                                                                                                                                                                                                                                                                                                     126;
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nucleic acid
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0 S. Wacker Drive, 32nd Floor
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Pred. No. 1.6e-13;
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US-09-416-833-8
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US-09-081-395-8
         Sequence 8, Application US/09416833 Patent No. 6197521 GENERAL INFORMATION:
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Best Local Similarity
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LENGTH: 289 base pairs
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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APPLICANT:
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                                                                                                                                                                                                            NAME: NO. 6083746nan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, IRRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,395
FILING DATE: 18-MAY-1998
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                     92 CTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAG 151
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STATE: Illinois
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                                                                                                                   GTGCTGAGGTGCAGTGCAGCTGCAACATCTTC 289
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E: cDNA
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Pred. No. 1.6e-13;
0; Mismatches 89;
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NUMBER OF SEQUENCES
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PCT-US95-02521-8
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                                                                         Sequence 8, Application PC/TUS9502521 GENERAL INFORMATION:
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Matches 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: No. 6197521nan, Kevin
REGISTRATION NUMBER: 35,303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION:
TITLE OF INVENTION:
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TITLE OF INVENTION:
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LENGTH: 289 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA: APPLICATION NUMBER:
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                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 312-715-1000
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                                                                                                                                                                                                                                                                                                                                                                                92 CTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGCTGGTGCTAAAATAG 151
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STATE: Illinois
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/416,833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                               GGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTAC 246
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26; Conservative
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10 S. Wacker Drive, Suite 3000
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Suppressor Elements and Genes Associated with Malignant
Growth in Cancer Cells
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Methods for Identifying Genetic
Suppressor Elements and Genes As
Growth in Cancer Cells
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Pred. No. 1.6e-13;
0; Mismatches 89
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                       Associated with
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Best Local Similarity
Matches 126; Conserv
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                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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ATTORNEY/AGENT INFORMATION:
NAME: NO. 5753432nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-C
TELECOMMUNICATION INFORMATION:
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LENGTH: 289 base pairs
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MEDIUM TYPE:
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TITLE OF INVENTION:
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                                                                                     APPLICATION NUMBER: FILING DATE: 04-MAF CLASSIFICATION: 435
                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                       STREET: 10 S. CITY: Chicago
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OPERATING SYSTEM: PC-DOS/MS-DOS
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STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                      Illinois
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10 S. Wacker Drive, Suite 3000
                                                                                                                                                                                                                                                                    USA
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N: 435
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Suppressor Elements and Genes
Growth in Cancer Cells
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Pred. No. 1.
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RESULT 15
US-09-081-167A-6
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Best Local Similarity
Matches 126; Conserv
                                                                                              ATTORNEL/AUGUSTA, CONTROL E NAME: NO. 6083745nan, Kevin E REGISTRATION NUMBER: 35,303 REFERENCE/DOCKET NUMBER: 93,3 TELECOMMUNICATION INFORMATION: TELEPHONE: 312-913-0001
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                    NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/081,167A
FILING DATE: 18-MAY-1998
CLASSIFICATION: 435
CLASSIFICATION: 435
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CITY: Chicago
TTATE: Illinois
TTSA
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MEDIUM TYPE: Floppy disk
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ITLE OF INVENTION:
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TOPOLOGY: 11
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                                                                                                                                             93,354-KK
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Pred. No. 3.5e-12;
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Genes As
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; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-09-081-167A-6
                                                                                                                                                                                                             Query Match 5.3%;
Best Local Similarity 56.8%;
Matches 126; Conservative
184 CGCATTGCTGCCTGCGCATGACCGTGGAGACTGCTGTTCTCATTGAGACTCTCGTG 243
                                                                     124 ATGCCAGGGTTGATGCGCATGCGGGAGATGTACTCAGCCTCCAAGCCACTGAAGGGTGCT 183
                                                                                                                               85 ATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGCTGGTGCT 144
                                                                                                                                                         Score 68.4; DB 3; Length 285; Pred. No. 3.5e-12; 0; Mismatches 96; Indels
                                                                                                                                                                                                          ; Gaps
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Search completed: April 21, 2003, 04:34:47 Job time : 2035.93 secs

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GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.
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Scoring table:	Title: Perfect score: Sequence:	Run on:	OM nucleic - nu
IDENTITY_NUC Gapop 10.0 , Gapext 1.0	US-09-782-051-1_COPY_549_1844 1296 1 tccaagggcagcagcaatttaacctaattattacagatac 1296	April 21, 2003, 02:39:45; Search time 259.419 Seconds (without alignments) 5018.577 Million cell updates/sec	OM nucleic - nucleic search, using sw model

Searched: 639749 seqs, 502280978 residues
Total number of hits satisfying chosen parameters: 1279498

Minimum DB seg length: 0
Maximum DB seg length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: Published_Applications_NA:*

1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodata/2/pubpna/PCT.NEW_PUB.seq:*

3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*

4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*

5: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*

7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

8: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*

9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

11: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*

12: /cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*

13: /cgn2_6/ptodata/2/pubpna/US00_NEW_PUB.seq:*

14: /cgn2_6/ptodata/2/pubpna/US00_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

بوبوبوب	c 13	-	Result
168.2 5 158 7 150.8 138.4	186 2 174 3 172.4 1 172.4		Score 1296 461.4
		31.0 2200 31.0 2429 36.0 384 18.6 1461 17.4 1422 17.4 1457	
433 721 382 284 284	720	34200 34200 3577	gth DB 5563 1 553 1
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US-09-960-352-4421 US-09-925-300-439 US-09-960-352-1149 US-09-920-300A-1423 US-10-033-528-1423	US-09-746-660A-101 US-09-738-626-838 US-10-037-598-26 US-09-754-853A-4	US-09-925-301-217 US-10-044-090-344 US-99-880-107-346 US-09-759-990-1 US-09-738-626-836 US-09-746-660A-97 US-09-746-660A-97 US-09-746-660A-97	ID US-09-782-051-1 US-09-867-701-2023 US-09-879-536-850
Sequence 4421, Ap Sequence 439, App Sequence 11499, Ap Sequence 1423, Ap Sequence 1423, Ap	Sequence 101, App Sequence 838, App Sequence 26, Appl Sequence 4, Appli	21 34 34 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,	Description Sequence 1, Appli Sequence 2023, App

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US-09-960-352-10555	US-09-878-574-9524	US-09-799-946-6	US-09-960-352-2035	US-09-799-946-8	US-09-960-352-5161	US-09-770-445-679	US-09-960-352-2551	US-09-960-352-12043	US-09-878-574-838	US-09-960-352-7284	US-09-960-352-1365	US-09-923-876-477	US-09-960-352-14145	US-09-770-149-117	US-09-960-352-10073	US-09-738-626-837	US-09-966-881-9	US-09-960-352-7006	US-09-960-352-12928	us-09-998-598-2191	US-10-017-754-1179	US-09-849-626-1179	US-09-902-941-1179	US-09-736-457-1179	US-09-960-352-9160
 Sequence 10555, A	Sequence 9524, Ap	Sequence 6, Appli	Sequence 2035, Ap	Sequençe 8, Appl1	Sequence 5161, Ap	Sequence 679, App	Sequence 2551, Ap	Sequence 12043, A	Sequence 838, App	Sequence 7284, Ap	Sequence 1365, Ap	Sequence 477, App	14145	Sequence 117, App	Sequence 10073, A	Sequence 837, App	Sequence 9, Appli	Sequence 7006, Ap	Sequence 12928, A	Sequence 2191, Ap	Sequence 1179, Ap	Sequence 1179, Ap	Sequence 1179, Ap	Sequence 1179, Ap	Sequence 9160, Ap

ALIGNMENTS

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	1200	41 CAGGATGTGTACTTGCTTAGGAAAATGGAATACGTTGCCAGCTTGCCATCTGCCA	0у 11
	1688	TO I GCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGGGATACAAG	Db 16
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	1628	21 GAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCATCACA	Qy . 10
•	1568	TACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCTCCTGGC	Db 15
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	8	41 GTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGG	
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	4	81 AAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAA	<
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	1268	09 TATGGTGAGGTAGGCAAGGGCTGCTGTGCTCTCAAAGCTCTTGGAGCAATTGTCTA	ப
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	1208	ATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTG	Db 11
	660	GTGATGTTTGGTGGG	Оу 6
	1148	HTTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCCGACGAATC	Db 10
	600	GATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTT	Qy 5
	1088	29 GTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACGTC	Db 10
	540	TTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTTCCGGCCATGAACGT	Qy 4
	1028	69 AAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGAAGAGAGCGTGACTGGT	Dp 9
	480	gaagtatecaáacgtgtttaagaagateegaggcattgtggaagagagegtgaetg	Qy 4
	968	09 GATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACTGGGTTTAT	Db 9
	420	ATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGGAGACTTAACCCACTGGGTTT	Ωу .
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	728	69 GGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACACACATCACCACCACCAGACA	р _р 6

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; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(553)
; OTHER INFORMATION: n = A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 2023
LENGTH: 553
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 35.6
Best Local Similarity 97.3
Matches 510; Conservative
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APPLICANT: Aglate, Paul A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1261 AAAAATGGGCCATTCAAACCTAATTATTACAGATAC 1296
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                   GACTCAACAAAAATGGGCCATTCAAACCTAATTATTACAGATAC
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TITLE OF INVENTION: NOVEL HUMAN GENES AND GENESTITLE OF INVENTION: NOVEL HUMAN GENES AND GENESTITLE OF INVENTION: PRODUCTS

FILE REFERENCE: CCD-257 (US)

CURRENT APPLICATION NUMBER: US/09/879,536

CURRENT FILING DATE: 2001-09-21

PRIOR APPLICATION NUMBER: US 60/088,801

PRIOR FILING DATE: 1998-06-10

NUMBER OF SEQ ID NOS: 850

SOFTWARE: FRASTSEQ for Windows Version 3.0

SEQ ID NO 850

LENGTH: 636

TYPE: DNA
RESULT 4

US-09-925-301-217

; Sequence 217, Application US/09925301

; Patent No. US20020052308A1
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APPLICANT:
APPLICANT:
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APPLICANT: Steinmann, Kathl
APPLICANT: Astle, Jon H.
APPLICANT: Burgess, Christo
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LOCATION: (1)...(636)
OTHER INFORMATION: n = A,T,C or
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                                                                                           TCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGT 577
                                                                                                                                               TTGTGGAAGAGAGGGGGAGCTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGC
                                                                                                                                                                                                 GAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCA 457
                                                                                                                                                                                                                                                                                          CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGT
                                                                                                                                                                                                                                                                                                                     CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGCCGAGTCAGAAGATGACTTCTGGTGGT 337
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                                                                                                                                                                                      GAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCA
                                                                              TCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGT
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Monahan, John E.
Schlegel, Robert
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Bushnell, Steven E.
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Pred. No. 5.2e-128;
0; Mismatches 1;
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; OTHER INFORMATION: n equals a,t,g, or US-09-925-301-217 SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 217 GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106 CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694 ORGANISM: Homo sapiens NAME/KEY: misc_feature LOCATION: (2188) 168 GCCTGATGCGTATGCGGGAGCGGTACTCGGCCTCCAAGCCACTGAAGGGCGCCCGCATCG 32 ACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTG CTCTCAAAGCTCTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGC GAGGCATTGTGGAAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTG TIGGTGGGAAACAAGIGGTGGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTGCTG GGATCCTCAAGGTGCCTGCCATCAATGTCAATGACTCCGTCACCAAGAGCAAGTTTTGACA ATGGGGGAGACTTAACCCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCC TGTGGTGCATTGAGCAGACCCTGTACTTCAAGGACGGGCCCCTCAACATGATTCTGGACG GGTGGTGTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATG CCATTGCCAAGGCTGGCATTCCGGTGTATGCCTGGAAGGGCGAAACGGACGAGGAGTACC CACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCT 331 GTGCTGAGGTGCAGTGCTCCAGCTGCAACATCTTCTCCACCCAGGACCATGCGGCGGCTG CTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGCTGGTGCTAAAATAG ACATCGGCCTGGCTGGGGGACGCAAGGCCCTGGACATTGCTGAGAACGAGATGCCGG CCCTGCGGGGTTTCGGAGCCCGCGTCATCATCACCGAGATTGACCCCATCAACGCACTGC ACCTCTATGGCTGCCGGGAGTCCCTCATAGATGGCATCAAGCGGGCCACAGATGTGATGA ACTTGTACTGCTGCCGAGAATCCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGT 631 GGAAGCTCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATA 571 GAGGCATCTCTGAGGAGACCACGACTGGGGGTCCACAACCTCTACAAGATGATGGCCAATG ACGGGGGCGACCTCACCAACCTCATCCACACCAAGTACCCGCAGCTTCTGCCAGGCATCC CTGGCTGCCTGCACATGACCGTGGAGACGGCCGTCCTCATTGAGACCCTCGTCACCCTGG TTGCCGGCAAGGTAGCGGTAGCAGGCTATGGTGATGTGGGCCAAGGGCTGTGCCCAGG Conservative 31.0%; 0, Score 402.4; DB 10 Pred. No. 2.6e-126; 0; Mismatches 521; DB 10; Length 2200 9 Gaps 751 691 511 451 391 407 151 167 91 827 767 707 647 467 347 271 287 227 587 527 211

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1245 TGG	d d	QY 92 CTCTGATTTCACTCAGGAAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTGAAATAG 151	
1169 TGG	Qy		
1188 AGC	дb		
1109 AAC	Qy	Matches 741; Conservative 0; Mismatches 521; Indexs 6; Gaps 2;	
1128 TGG	В	ery Match 31.0%; Score 402.4; DB 12; Length 2429; St Local Similarity 58:4%; Pred. No. 2.8e-126;	
1052 CAG	Qγ	21 OP 21 10 10 10 10 10 10 10 10 10 10 10 10 10	
1068 AGA	В		
992 CAG	Qy		
1008 TCA	ДĎ		
932 TCC	Ωy	344	
948 AGG	рь	NUMBER OF SEQ ID NOS: 850	
872 AAA	Оу	CHERENT APPLICATION NUMBER: US/10/044,090	
888 TCT	Дb	TITLE OF INVESTIGN: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION DESCRIPTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION	
812 TCG	Ωу	; FACERAL INFORMATION:	
828 AGG	ďď	Sequence 344, Application US/10044090	
752 .AGG	δĀ	RESULT 5	
768 ccc:	Дb		
692 CTC	Qy		
708 TTG	Дb	1303 CTGHGANGCANGCCCNGIACCIGGGCHIGICCIGIGHIGHIGGCCCCIICANGCCGGNICACI	
632 TTG	Qy	######################################	
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572 ACT	γо	1169	
588 GGA:	당	AGCTGTGGACCCATCCAGACAAGTACCCCGTTGGGGTTCATTTCCTGCCCAAGAAGC	
512 GGA/	Qy	1109 AACTCTATAATGCACCCGAGGGGCGATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAA	
528 GAG	Дb	1128 TGGGCCACCCCAGCTTCGTGATGAGTAACTCCTTCACCAACCA	
452 GAG	Qy	CAGTTCCCACCTTTGTTCTGTCCACAGCCACAACACAGGCTTTGGCACTGATAG	
468 ACGC	Db	Db 1068 AGAATGGGCGCCGCATCATCCTGCCTGGCCGAGGGTCGGCTGGTCAACCTGGGTTGTGCCA 1127	
392 ATG	Qγ		
408 TGTG	D	Db 1008 TCAACGAGAACGCCGTGGAGAAGGTGAACATCAAGCCGCAGGTGGACCGGTATCGGTTGA 1067	
332 GGT0	γo		
348 CCAT	당	Db 948 AGGATGATGCCATTGTGTGAACATTGGACACTTTGACGTGGAGATCGATGTCAAGTGGC 1007	
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	ᄝ	Db 888 TCTTTGTCACCACCACAGGCTGTATTGACATCATCCTTGGCCGGCACTTTGAGCAGATGA 947	
	Qy	OY 812 TOGTAATAACTTGCACAGGAAATAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGA 871	
	문 :	Db 828 AGGCTGCCATGGAGGCTATGAGGTGACCACCATGGATGAGGCCTGTCAGGAGGGCAACA 887	
152 TGGG	o _y	QY 752 AGGCCTGCATGGATGGGTTCAGGGTGGTAAAATGAAGTCATCCGGCAAGTCGATG 811	
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GATGAGGCAGTGGCTGAAGCCCCACCTGGGCAAGCTGAATGTGAAGTTGACCAAGCTAA 1304
                                  GATGAATACGTTGCCAGCTTGCCATCCATCATTTGATGCCCACCTTACAGAGCTGA 1228
                                                                                                                                                      CTCTATAATGCACCCGAGGGGGGGATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAA 1168
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            RESULT 7
US-09-759-990-1
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Sequence 1, Application US/09759990
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 381;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 346, Application Patent No. US20020142981A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
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SEQ ID NO 346
LENGTH: 384
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                  GCAAGTCGATGTCGTAATAACTTGC
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Scherf, Uwe
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Pred. No. 1.9e-104;
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; OTHER INFORMATION: Nucleotide sequence encoding SAHH US-09-759-990-1
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GENERAL INFORMATION:
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TITLE OF INVENTION: HIGH EXPRESSION AND PRODUCTION OF HIGH
TITLE OF INVENTION: SPECIFIC ACTIVITY RECOMBINANT S-ADENOSYLHOMOCYSTAINASE
TITLE OF INVENTION: (SAHH) AND IMPROVED ASSAYS FOR S-ADENOSYLMETHIONINE (SAM)
FILE REFERENCE: 31276-20026.00
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                                                                                                                                                                                                                                                                                        1093 ATGAAATACCCAGGCATCAAGCACATCCCAATCAAGCCAGAATACGACATGTGGGAA†TC
                                                                                                                                                                                                                               991 CCAGATGGCAAACGAGTTGTCCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCC 1050
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GAACTCTATAATGCACCCGAGGGGCGATACAAGCAGGATGTGTACTTGCTTCCTAAGAAA 1167
                                                                                                                                                                       CCAGATGGCCACGCTATCCTCCTTCTTGCTGAGGGCCGCCTTCTTAACCTTGGCTGCGCT
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Publication No. US20020197605A1
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SOFTWARE: PatentIn ver. 3.0
SEQ ID NO 836
LENGTH: 1422
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CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99:377484
PRIOR FILING DATE: 1999-12-16
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PRIOR FILING DATE: 2000-04-07
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 763 GATGGGTTCAGGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACT 822
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                                                                                                             AACGTGCTTGTCTGCGGTTACGGCGATGTCGGCCAAGGGCTGCGCTGAGGCTTTCGACGGC
                                                                                                                                            CAAGTGGTGGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGCTGCTGCTCTCAAAGCT 702
                                                                                                                                                                         ACCCGCCACTGCCTGATCGACGGCATCAACCGCGCCACTGACATGCTCATGGGCGGCAAG 765
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SENOH, AKIHIRO
IKEDA, MASATO
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OCHIAI, KEIKO
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                                                                    PRIOR FILING DATE: 1999-06-25
PRIOR APPLICATION NUMBER: 60/142101
PRIOR APPLICATION NUMBER: 60/148613
PRIOR FILING DATE: 1999-08-12
PRIOR FILING DATE: 1999-08-12
PRIOR APPLICATION NUMBER: 60/187970
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR APPLICATION NUMBER: DE 19931420.9
PRIOR FILING DATE: 1999-07-08
SOFTWARE: P
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APPLICANT: Kroger, Burkhard
                                                    NUMBER OF SEQ ID NOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: HWANG, BYING-JOON
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CP2
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APPLICATION NUMBER: 09/03124
FILING DATE: 2000-06-23
APPLICATION NUMBER: 60/141031
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inch, 1.44 Mb floppy disk

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RESULT 10
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; Sequence 1, Application US/10021121
; Patent No. US20020112444A1
; GENERAL INFORMATION:
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Pred. No. 4.9e-66;
0; Mismatches 354;
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                                                                                                                                                                                                                                                                                                                                                                Matches 190;
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
                      1266
                                                                                                          1326
                                                                                                                                                                                            1386
                                                                                                                                                                                                                                      795
                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: TOICH1a, PhD., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Caras, Ingrid W
TITLE OF INVENTION: A2-1 Neuzotrophic Factor
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
                                                                AATCGATGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1877 base pairs
TYPE: Nucleic Acid
STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/10/021,121 FILING DATE: 06-Dec-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/635,130 FILING DATE: 19-Mar-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY:
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IDENTIFICATION METHOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IDENTIFICATION METHOD
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Linear

Extra Cellular Domain

signal peptide

Length 1877;

0

Transmembrane 901-978

Domain

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1446 CCCCATCTGTGCTCTGCAGGCCTGCATGGATGGGTTCAGGGTGGTAAAGCTAAATGAAGT 1387
                                                                                                                                                                                                                                      735 CCCCATCTGTGCTCTGCAGGCCTGCATGGATGGGTTCAGGGTGGTAAAGCTAAATGAAGT 794
AATCGATGTG 1257
                                                            CATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATGTAGTGACACGGGA 854
                                                                                                   GCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACACAGA 914
                                                                                                                                                                                                                                                                      Conservative
                              924
                                                                                                                                                                                                                                                                                      14.7%;
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                                                                                                                                                                                                                                                                                    Score 190; DB 12; Pred. No. 7.9e-54;
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US-09-746-660A-101
US-09-746-660A-101
; Sequence 101, Application US/09746660A
; Publication No. US20030049804A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: CDS
LOCATION: (101)..(1396)
OTHER INFORMATION: FRXA01371
S-09-746-660A-101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity Matches 377; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Vers. 2.0 SEQ ID NO.101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/746,660A CURRENT FILING DATE: 2000-12-22 PRIOR APPLICATION NUMBER: 09/606740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RPPLICANT: HWANG, BYUNG-JOON
IITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
IITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-121CP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH: 1396
                                                                                                                                                                                                                                                                        818 ACCCGCCACTCCCTGATCGACGGCATCAACCGCGCCACTGACATGCTCATGGGCGGCAAG 877
                                                                                                                                                                                                                                                                                                                                                                                            523 GTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGC 582
866
                                                                                     938 CAGGGCGCTCGCGTCAAGGTCACCGAAGCTGACCCAATCAACGCTCTTCAGGCTCTGATG
                                                                                                                                                                                                                        643 CAAGIGGTGGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTGCTGCTCTCAAAGCT 702
                                                                                                                                                                                                                                                                                                                   583 TGCCGAGAATCCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAA 642
                                                                                                                                                                                                                                                                                                                                                             758 TTCCCAGCGATGAACGTCAACGACGCTGTCACCAAGTCCAAGTTTGATAACAAGTACGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                     698 GAGGAAACCACCACCGGTGTGCACCGCCTGTACCACTTCGCTGAAGAAGGCGTGCTGCCT 757
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                463 GAAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGT 522
                                          763 GATGGGTTCAGGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACT 822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 1999-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/141031 FILING DATE: 1999-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 09/603124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: DE 19931420.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: 2000-06-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 60/187970
                                                                                                                                                                                AACGTGCTTGTCTGCGGTTACGGCGATGTCGGCAAGGGCTGCGCTGAGGCTTTCGACGGC 937
GATGGCTACTCTGTGGTCACCGTTGATGAGGCCATCGAGGACGCCGACATCGTGATCACC 1057
                                                                                                                              CTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kim, Jun-Won
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zelder, Oskar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Schroder, Hartwig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kroger, Burkhard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee, Heung-Schick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Haberhauer, Gregor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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Pred. No. 1.5e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1396;
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US-09-738-626-838/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           ; ORGANISM: Corynebacterium glutamicum US-09-738-626-838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Pat
SEQ ID NO 838
LENGTH: 720
                                                                                                                                                                                                                                                                                                                                                              Query Match 13.4%;
Best Local Similarity 61.0%;
Matches 282; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITLE OF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1118 CTGCTGGGCAACATCGGTCACTTTGATAATGAGATCGATATGCATTCCCTGTTGCACCGC 1177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1058 GCGACCGGCAACAAGGACATCATTTCCTTCGAGCAGATGCTCAAGATGAAGGATCACGCT 1117
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                                                                                                                                                                                 405
                                                                                                                                                                                                                523 GTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACCTTGTACTĞC 582
                                                                                                                                                                                                                                                                                                    463 GAAGAGACCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGT 522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  940 CCGGAGCTGACGTGGGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGC 999
                                           643 CAAGTGGTGGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGCTGCTGCTCCAAAGCT 702
                                                                                      345
                                                                                                                                 583 TGCCGAGAATCCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAA 642
                                                                                                                                                                                                                                                                          465 GAGGAAACCACCACCGGTGTGCACCGCCTGTACCACTTCGCTGAAGAAGGCGTGCTGCCT 406
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                                                                                      ACCCGCCACTCCCTGATCGACGGCATCAACCGCGCCACTGACATGCTCATGGGCGGCAAG
                                                                                                                                                                                 TTCCCAGCGATGAACGTCAACGACGCTGTCACCAAGTCCAAGTTTGATAACAAGTACGGC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CGCTCCATCATCGTCCTGTCCGAAGGTCGCCTGTTGAACCTTGGCAACGCCACCGGACAC 1297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAACGAGTTGTCCTCGCAGAGGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCC 1059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATCGTATGCAATATGGGCCACTCCAACACAGAAATCGATGTGACCAGCCTC---CGCACT 939
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACC - - - TTTGTTCTGTCCATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INVENTION: NOVEL POLYNUCLEOTIDES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PatentIn ver. 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HAYASHI, MIKIRO
OCHIAI, KEIKO
YOKOI, HARUHIKO
TATEISHI, NAOKO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MIZOGUCHI, HIROSHI
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o. US20020197605A1
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                                                                                                                                                                                                                                                                                                                                                                                   Score 174; DB 9;
Pred. No. 1.3e-48;
                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                             Length 720;
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US-10-037-598-26
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US-10-037-598-26
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Patent NO. US20020157143A1

GENERAL INFORMATION:

APPLICANT: Monsanto Co
APPLICANT: Concibido, Vergel
APPLICANT: Concibido, Vergel
APPLICANT: Delanney, Xavier

TITLE OF INVENTION: Soybean Plants with Enhanced Yields and Methods for Breeding:
TITLE OF INVENTION: Screening of Soybean Plants with Enhanced Yields

FILE REFERENCE: 38-21(52175)B

CURRENT APPLICATION NUMBER: US/10/037,598

CURRENT FILING DATE: 2002-01-04

PRIOR APPLICATION NUMBER: 06/260,040

PRIOR FILING DATE: 2002-01-05

NUMBER OF SEQ ID NOS: 37
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LENGTH: 3830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     883 ATCGTATGCAATATGGGCCACTCCAACACAGAAATCGATGTG 924
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
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 CTTTGACAATGAGATCGACATGCTTGGGCTGGAGAACTACCCCGGCGTGAAGCGCATCAC 3481
                                                                                                                                                                                                                                                                  TGCACAGGAAATAAGAATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGT
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                                   CTCCAACACAGAAATCGATGTGACCAGCCTCCGCACT---CCGGAGCTGACGTGGGAGCG
                                                                         CATCATGGTTGACCACATGAGGAAAATGAAGAACAATGCCATTGTTTGCAACATTGGTCA
                                                                                                                                                    CTTGGAGGATGTTGTTCTGAGGCTGATATCTTTGTCACCACCACCGGTAACAAGGACAT
                                                                                                                                                                                         GCTHAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATGT 842
                                                                                                                                                                                                                               GACCGAGATTGATCCCATCTGTGCCCTTCAGGCTCTCATGGAAGGCCTTCAGGTTCTGAC
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                                                                                                                                                                                                                                                                                                        TGGTGATGTTGGCAAGGGTTGTGCTGCTGCAATGAAGCAGGCTGGTGCTCGTGTCATCGT
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US-09-754-853A-4/c
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Wang, Ming Li
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules
TITLE OF INVENTION: Soybean Cyst Nematode Resistance
FILE REFERENCE: 38-10(15810)B
CURRENT APPLICATION NUMBER: US/09/754,853A
CURRENT FILING DATE: 2001-01-05
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR APPLICATION NUMBER: US 60/174,880
PRIOR FILING DATE: 2000-01-07
NUMBER OF SEQ ID NOS: 1119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Hauge, Brian m.
APPLICANT: Parnell, Laurence D.
APPLICANT: Parsons, Jeremy D.
                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: unsure
LOCATION: (1)..(513509)
OTHER INFORMATION: unsure at all n locations
OTHER INFORMATION: Clone ID: 318013_region_A3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: (111805)..(113968),(114684)..(115204)
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                                                                                                                                         TGGCCTGAAGAGGACCACAGATGTGATGTTTTGGTGGGAAACAAGTGGTGGTGTGTGGCTA
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  TGGTGATGTTGGCAAGGGTTGTGCTGCTGCAATGAAGCAGGCTGGTGCTCGTGTCATCGT
                                                             TGGTGAGGTAGGCAAGGGCTGCTGTGCTGCTCAAAGCTCTTGGAGCAATTGTCTACAT 722
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Pred. No. 2.5e-46;
0; Mismatches 331;
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                                                                                                                                                                                                                                                                               ; TYPE: DNA
; ORGANISM: Bos taurus
; OTHER INFORMATION: Clone ID: 19-LIB34-025-Q1-ET-E3
US-09-960-352-4421
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Db 178258 CAGTGTGCCTGTTGAGGGTCCATACAAGCCTGCTCACTACAGGTAC 178213
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                                                                                                                                                                                      Query Match (6)
Best Local Similarity
Matches 254; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: NUCLEIC ACID AND OTHER MOLECULES ASSOCIATED WITH LACTATION AND TITLE OF INVENTION: MUSCLE AND FAT DEPOSITION

FILE REFERENCE: 16511.006/37-21(10298)C

CURRENT APPLICATION NUMBER: US/09/960,352

CURRENT FILING DATE: 2001-09-24

NUMBER OF SEQ ID NOS: 15112

EQ ID NO 4471
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atent No. US200201
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                                                                                             GAGACCCTCGTTGCCCTGGGTGCTGAGGTGCGGTGGTCCAGCTGCAATATCTTCTCCACC 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TCACCTGGGCAAACTTGGAGCTAAGCTGACCCAGCTTAGCAAGTCCCAGGCTGATTACAT 17825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCATCTGCCATCATTTGATGCCCACCTTACAGAGCTGACAGATGACCAAGCAAAATATCT 1250
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                              ACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAG
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                                                            TACAAGATGATGGCCAAAGGGATCCTGAAGGTGCCGGCCATCAATGTCAATGACTCTGTC
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Search completed: April 21, 2003, 07:31:10 Job time: 854.419 secs

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Result
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Maximum Match 100%
Listing first 45 summaries
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                                 845.6
834.8
775.6
732.2
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59373	BQ05937		102	5	œ	34
53920	BM45392		98	5	86.	33
62203	ВQC		112	5	•	32
92477 602	BF79247		94	5	88.	31
51644 AV7	AV75164		66	5	88.	30
14546	·BQ61454		59	5	59	29
95818	BM99581		64	5	93.	28
58506	AW95850		63	5	97.	27
59448	BG25944		96	5	599.8	26
42285	BE54228		81		8	25
37761	BM83776		61,	7.	_	24
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697210	BG69721		74	5	16.	7
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ALIGNMENTS

FEATURES Source		-								COMMENT	JOURNAL	TITLE	AUTHORS	REFERENCE			ORGANISM	SOURCE	KEYWORDS	VERSION	ACCESSION		DEFINITION	Locus	BM449470	7.00CE
Location/Qualifiers	High quality sequence stop: 694.	Plate: LLAM12117 row: m column: 06	round through the L.M.A.G.E. Consortium/LLNL at:	Clone distribution: MGC clone distribution information can be	DNA Sequencing by: Agencourt Bioscience Corporation	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)	cDNA Library Preparation: Life Technologies, Inc.	Tissue Procurement: ATCC	Email: cgapbs-remail.nih.gov	Contact: Robert Strausberg, Ph.D.	Unpublished (1999)	National Institutes of Health, Mammalian Gene Collection (MGC)	NIH-MGC http://mgc.nci.nih.gov/.	1 (bases 1 to 1042)	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	<pre>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</pre>	Homo sapiens	human.	EST.	BM449470.1 GI:18498510	BM449470	5', mRNA sequence.	AGENCOURT_6400881 NIH_MGC_67 Homo sapiens cDNA clone IMAGE:5493677	linear		
				can be		NI)						n (MGC)			no.	eleostomí;							AGE: 5493677	EST 05-FEB-2002		

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BASE COUNT
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             TAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGA
                                                                              GATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGC
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/db_xref="taxon:9606"
/clone="IMAGE:5493677"
/clone=lib="NIH_WGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH108 (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Lif
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309 g 240 t 7 others
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; Pred. No. 6.9e
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                                       Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Alzawa, K., Izawa, M., Nishi, K., Kiyosawa, H., Kondo, S., Yamanaka, I., Saito, T., Okazaki, Y., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavaht, T., Fleischmann, W., Gasaterland, T., Gissi, C., King, B., Kochiwa, H., Kuehi, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Quackenbush, J., Schriml, L.M., Staubli, F., Suzuki, R., Tomita, M., Wagner, L., Washlo, T., Sakai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M.F., Brownstein, M.J., Bult, C., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kaniya, M., Lee, N.H., Lyons, P., Marchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Sasaki H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K. F., Suzuki, H., Wand, H., Weitz, C., Whittaker, C., Wilming, L., Wand, H., Weitz, C., Whittaker, C., Wilming, L., Wand, H., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y. Storch, K., F., Suzuki, S., and Hayashizaki, Y., Storch, K., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y., Storch, K., F., Suzuki, S., and Hayashizaki, Y., Storch, K., F., Suzuki, S., and Hayashizaki, Y., Soshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S., and Hayashizaki, Y.
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                                                             Arakawa, T., Baldarelli, R., Bono, H., Brownstein, M., Bult, C., Carninci, P., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiramoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishii, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, N., Kohii, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, H., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Saito, H., Saito, R., Sakai, C., Sakai, K., Shinaka, T., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagama, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamanura, T., Yamanaka, I., Yashila, A., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemonic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rot = 100.0. Second strand cDNA was prepared with the primer adapter of sequence [5' adapta and XhoI. cDNA of size comprised longer than 7 kb was selected before cloning. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I. Cloning sites, 5' end: SalI; 3'
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further details.
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                                                                                                                                                                                                                                                                                                                                                                                                           /tissue_type="skin"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
/dev_stage="0 day neonate"
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                                     AAGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGCTTGCATCTG 1197
                                                                                                                                                                                                                            CAGA-GGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCATC 1077
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

Tissue Procurement: Miklos Palkovits, M.D., Ph.D.

cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shira

Toshiyuki and Piero Carninci (RIKEN)

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
plate: LLAM10674 row: b column: 11

High quality sequence: stop: 839.
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                    TGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACGT
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian
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                                                                                                                                                     Similarity
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4793770"
/clone_lib="NIH_MGC_96"
/tissue_type="hypothalamus"
/lab_host="DH10B"
                                                                                                                                                                                               ocation/Qualifiers
                                                                                                                                                    59.8%;
98.5%;
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AGENCOURT_8715624 NIH_MGC_101
5', mRNA sequence.
B0896777
                  CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLN DNA Sequencing by: Agencourt Bloscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://image.lnl.gov
Plate: LLCM2608 row: d column: 14
                                                                                                                                                                          Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                   Unpublished (1999)
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National Institutes of Health, Mammalian
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                            AGGGTCGTCTACTCAATTTGAGCTGCTCCACAGGTTCCACCTTTGTTCTGTCCATCACAG
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/lab_host="DH10B (phage-resistant)"
/note="Organ: lung; Vector: pOTB7; Site_1: EcoRI; Site_2:
/khoI; cDNA made by oligo-dT priming, Directionally cloned
into EcoRI/KhoI sites using the following 5; adaptor:
GGCACGAG(G). Library constructed by int Hone
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC_Library."
26 a 205 c 247 g 216 t
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/db_xref="taxon:9606"
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HRI human cDNA project (Ota,T., Wakamatsu,A., Ozawa,M., Ishii,S. Saito,K., Yamamoto,J., Nakamura,Y., Nishikawa,T., Nagai,T., Suzu,Y., Sugano,S., Isogai,T.)
Unpublished (2000)
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
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Tel: 81-438-52-3975
Fax: 81-438-52-3986
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1 (bases 1 to 748)
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/cell_line="NT2"
/cell_line=
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/db_xref="taxon:9606"
/clone="NT2RM4000853"
/clone_lib="NT2RM4"
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Pred. No. 1.3e-212;
0; Mismatches 5;
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                                                                                                                                                                                                                               Email: cgapbs r@mail.nih.gov
Tissue Procurement: Dr. James R. Lupski
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 93)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (Collection)
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AGENCOURT_8482604 Lupski_dorsal_root_ganglion
clone IMAGE:6185747 5', mRNA sequence.
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            /note-"Vector: pCMV-SPORT6 (Life Technologies); Si-
Not1; Site_2: Sal1; cDNA made by oligo-dT prining.
Directionally cloned using the following adaptors:
5'-TCGACCCACGCGTCCG-3' and
                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6185747"
                                                            /tissue_type="dorsal root
/dev_stage="adult, 36 yr"
/lab_host="DH10B"
                                                                                                   /sex="male"
                                                                                                           /clone_lib="Lupski_dorsal_root_ganglion"
  -GACTAGTTCTAGATCGCGAGCGGCCGCCCT(15)-3'.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia, Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 832)
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Tissue Procurement: Louis M. Staudt, M.D., Ph.D.
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
cDNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image linl.gov
Plate: LLCM69 row: n column: 07
High quality sequence start: 2
High quality sequence stop: 767.
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1532-3 Yana, Kisarazu, Cl
Tel: 81-438-52-3975
Fax: 81-438-52-3986
                                                                  HRI human cDNA project
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
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AU133711 OVARC1 Homo sapiens
Email: genomics@hri.co.jp
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Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. an
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/clone="ovaRC1000494"
/clone_lib="ovaRC1"
/clone_type="ovary, tumor tissue"
/tissue_type="ovary, tumor tissue"
/note="vector: pME18SFL3"
/note="vector: pME18SFL3"
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HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix Research Institute; cDNA library construction: Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.
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Contact: Takao Isogai
Genomics Laboratory
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HRI human cDNA project
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1 (bases 1 to 745)

Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
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/cell_line-"NT2"
/cell_line-"NT2"
/note-"Yecttor: pME18SFL3; mRNA from NT2 neuronal
/note-"Yecttor: NT2 neuronal
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/db_xref-"taxon:9606"
/clone-"NT2RP3003545"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: yongsung@mail:kribb.re.kr
Plate: 76 row: A column: 11
High quality sequence stop: 691.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Korea Research Institute of Bioscience & Biotechnology 52 Eceun-dong Yuseong-gu, Daejeon 305-333, South Korea Tel: +82-42-860-4470 Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Kim YS
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Kim, N.S., Hahn, Y.,
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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1 (bases 1 to 691)
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/note="Organ: Stomach; Vector: pME18-FL3; Site_1: xhoI; Site_2: xhoI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including SfiI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized with Superscript II using SfiI oligo-dT primer. After first strand synthesis, RNA was degraded by NaOH treatment and cDNA was amplified by PCR reaction. The PCR products were digested with SfiI and cloned into DraIII- digested ME185-FL3 vector. The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library: "

    Hahn, Y., Oh, J. H., Lee, J. Y., Ahn, H. Y., Chu, M. Y., Kim,
    Cheong, J. E., Sohn, H. Y., Kim, J. M., Park, H. S., Kim, S. a

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_type="Epithelial"
/cell_line="SNU-601"
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/db_xref="taxon:9606"
/clone="S9SNU601-76-A11"
/clone_lib="S9SNU601"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /lab_host="Top10F/"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1098)
NIH-MGC http://mgc.nci.nih.gov/.
Mational Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
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AGENCOURT_6402556 NIH_MGC_85
5', mRNA sequence
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TGACCAGCCTCCGCACTCCGG 943
                                                                                 ATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACACACAGAAATCGATG
                                                                                                                          AAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATGTAGTGACACGGGAGCACTTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information found through the I.M.A.G.E. Consortium/LLNL at: http://lmage.llnl.gov Plate: LLAM12127 row: k column: 19
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/Clone_lib="NIH_MGC_85"
/Clone_lib="NIH_MGC_85"
/tlssue_type="lymphoma, cell line"
/tlssue_type="lymphoma, cell line"
/tlssue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/lab_host="lymph; Vector: pcMV-SPORT6; Site_1: No. Site_2: SalI; Cloned unidirectionally; oligo-dT prim. Site_2: SalI; Cloned unidirectionally; oligo-dT prim. Average insert size 1.867 kb. Library enriched for full-length clones and constructed by Life Technolog. Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
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uence stop: 518.
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Pred. No. 7.7e-195;
0; Mismatches 5;
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BASE COUNT	FEATURES source	REFERENCE AUTHORS TITLE JOURNAL	ACCESSION VERSION KEYWORDS SOURCE ORGANISM	RESULT 14 AL527928 LOCUS DEFINITION	Qy 874 Db 779	Оу 814 рь 719	Qy 755 Db 659	Qy 695 Db 601	Oy 637 Db 541	Oy 577	Qy 517 Db 421	Qy 457 Db 361
	Genoscope BP 191 91 Email: se	Eukaryota; Metazoa; Mammalia; Eutheria; 1 (bases 1 to 938) Li,W.B., Gruber,C., Full-length cDNA 11 Unpublished (2001) Contact: Genoscope	-	AL527928 AL527928 LTI_	AACAGTIGTATCGTATGCAATATGGGCCACTCCA 907	GTAATAACTTGCACAGGAAATAAGAATGTAGTGACACGGGAGCACTTGGATCGCATqAAA 873	CCTGCATGGATGGGTTCAGGGT-GGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTC 813	TCAAAGCTCTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTG¢AGG 754	GGGAAA-CAAGTGGTGGTGTGGGTATGGTGAGGTA-GGCAAGGGCTGCTGTGCTG	TACTGCTGCCGAGAATCCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGTTTGGT 636	CTOTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTG 576	ATTGTGGAAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAG 516

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REFERENCE
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TITLE
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ORGANISM
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Mammalia; Eutheria; Primates; Catai
1 (bases 1 to 930)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mam
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                         GTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCCATGAACGTC
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                                                                                                                      mRNA sequence.
BG751929
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602731492F1 NIH_MGC_43
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mo sapiens
                                                           Craniata; Vertebrata; Catarrhini; Hominidae;
                               Mammalian Gene Collection (MGC)
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s cDNA clone IMAGE:4874951 5',
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  AACTCTATAATGCACCCGAGGGGGGGATACAAGCAGGATGTGTACTTGC-TTCCTAAGAAA
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Query Match
Best Local S
Matches 756
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                                                                         CACAGTTCCCACCT-TTGTTCTGTCCATCACAGCCACAACACAGGCTTTGGCACTGATAG 1108
                                                                                                                                                                                                         CCAGATGGCAAACGAGTTGTCCTCCTGG-CAGAGGGTCGTCTACTCAATTTGAGCTGCTC
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//db_xref="taxon:9606"
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//note="Organ: eye; Vector: pOTB7; Site_1: xhoI; Site_2: pote="Inage: pote="Ina
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Pred. No. 1.8e-191;
0; Mismatches 27;
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780	1285	721	1225	661	1168	601
780 TATTACAGATA 790	1285 TATTACAGATA 1295	721 CTGACAGATGACCAGGCAAATATCTGGGGGACTCAGGAACACTGGG-CATTCAAACCTACT 779	1225 CTGACAGATGACCAAAGCAAAATATCTGGGACTCAACAAAAAATGGGCCCATTCAAAACCTAAT 1284	661 ATGGATGAATACGTTGGCCAGCTTTGCATCTGCCATCCAT	1168 ATGGATGAATACGTTGCCAGCTTGCCATCTGCCAT-CATTTGATGCCCACCTTACAGAG 1224	
		φ	84	0	24	0

Search completed: April 21, 2003, 03:59:07 Job time: 1760.62 secs

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Database :
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1844
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Copyright (c) 1993 - 2003 Compugen Ltd.
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QY 421 CCAAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCCTCACAGCTACA 480	Qy 181 GGGCAGGGGGGGCCAGAAGGGGGAAAAGAAGCGAGGGGGG	Query Match Best Local Similarity 100.0%; Score 1844; DB 6; Length 2563; Best Local Similarity 100.0%; Pred. No. 0; Matches 1844; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Qy 1 GGCGCGGGCAGGTCGGAGCTCGGAGCTGCTTCTGGTTCTCTTGTGGCCACCGTCGCT 60	to be identified." in_start=1 xref="g1:1019061" xref="g1:1019061	JOURNAL Patent: WO 9814562-A.1 09-APR-1998; HART DEREK NIGEL JOHN (NZ) FEATURES Location/Qualifiers 1. 2563 50urce 1.2563 60b_xret="taxon:9606" CDS
1501 GGGAGGAGAGGTTCTTGCTTAGATTGAACTGATATAATACGTTGCCAGGGGC 1561 TCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCCACAGTTCCCACACTTTGTTCTGT 1561 TCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGT 1561 TCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCCTTTGTTCTGT 1561 TCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCCTTTGTTCTGT 1621 CCATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGC 1611	Oy 1261 TIGTCTACATTACCGAAATCGACCCATCTGCTCTGCAGGCCTGCATGGTTCA 1320 1261 TIGTCTACATTACCGAAATCGACCCCATCTGTTGCTCTGCAGGCCTGCATGGTTCA 1320 1261 TIGTCTACATTACCGAAATCGACCCCATCTGTTGCTCTGAGGCCTGCATGGTTCA 1320 Qy 1321 GGGTGGTAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGATGATAACTTGCACAGGAA 1380	1021 TGACTGGTGTTCACAGGCTGTATCAGCTCTCAAAGCTGGGAAGCTCTTGTTCCGGCCACAGCTGTGTTCCGGCCACAGCTGTGTTCCGGCCACAGCTGTGTTCCGGCCACAGCTGTGTTCCGGCCACAGCTGTGTTCCGGCCACAGCTGTGTTCACAGCTGTGTTCACAGCTCTGTATCACAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCACAGCTTTGATAACTTGTACTGTTACCAAAGCTCTGTATCACAGAATTTGATAACTTGTACTGCTGCCGAGAATTCTGTTACCAAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATTCTGTTACCAAACAGAAGTTTGATAACTTGTACACAAACAGAATTGTACTGTACCAGAATTGTAACTTGTACCAAACAAA	781 CTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACCACTGGCTGG	Db 601 GACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAAC 660 Oy 661 GTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACACACATCACAG 720

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Dekker,J.W., Budhia,S.,
Hart,D.N.J. and Kato,M.
Direct Submission
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                                                                          /product="5-adenosylhomocysteine hydrolase-like protein"
/protein_id="AALZ6869,1"
/db_xref="G1:1658869;1"
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LIETLCALGAQCRWSACNIYSTQNEVAAALAEAGVAVFAWKGESEDDFWRGIDGCVNM
DGWQANMILDDGGDLTHWYKKYPNVFKKIRGIVEESVTGVHRLYQLSKAGKLCVPAM
NVNDSVTKQKFDNLYCCRESILDGLKKTDTDVMFGGKQVVVCGYGEVGKGCCAALKALG
AIVYITEIDFICALQACMDGFRVVKLMEVIRQVDVITCTGNKNVVTREHLDRKKNGC
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PTFVLSITATTQALALIELYNAPEGRYKQDVYLLPKKMDEYVASLHLPSFDAHLTELT
DDQAKYLGIKNNGPEFKNYYKY"
57 a 648 c 708 g 664 t
                                                                                                                                                                                                                                                                                                                          /note="DCAL; dendritic cell expressed AHCY-like protein; expressed in dendritic cells in blood, Langerhans cells and dermal dendritic cells; mRNA increased during monocyte differentiation to monocyte-derived dendritic cells in the presence of GM-CSF and IL-4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /chromosome="1"
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/cell_line="Hodgkin's disease cell line L428"
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                       Submitted (10-JUL-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                     Homo sapiens, S-adenosylhomocysteine hydrolase-like MGC:8936 IMAGE:3853747, mKNA, complete cds. BC010681 BC010681.1 GI:14715037
                                                                Strausberg, R. Direct Submission
                                                                                                                              Homo sapiens.
Homo sapiens
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                                                                                       Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
1 (bases 1 to 2583)
 Project URL:
http://mgc.nci.nih.gov
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                                                                                              GGGCCGGCGGGGAATGTCGATGCCTGACGCGATGCCGCTGCCCCGGGGTCGGGGAGGAGC
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  TGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGGCCACCGTCACCA
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                                                                                                                                                                                                                                                                                                                                                                                      GGCGCGGGCAGGTCGGAGCTCGGAGCTGCTTCTTGGTTCTTGTTGGCCGCCGTCGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Web site: http://www.hgsc.bcm.tmc.edu/cdna/Contact: villalon@bcm.tmc.edu.
Villalon, D.K., Luna, R.A., Hale, S.M., Hul
A.M., Holloway, M., Telford, B, Hodgson, A.
Muzny,D.M., Gibbs,R.A.
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CDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortiu
DNA Sequencing by: Baylor College of Medicine Hun
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Email: cgapbs-r@mail.nih.gov
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/clone-"MGC:8936 IMAGE:3853747"
/tissue_type-"Colon, adenocarcinoma"
/clone_lib-"NIH_MGC_65"
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LRKRAQGEKFILAGAKIYGCTHITAQTAVLIETLCALGAQCINGSCNIYSTQNEVAAAL
AEAGVAVFAWKGESEDDFWWCIDRCVNMDGWDAMMILDDGGDLTHWYKKY PNVFKKI
RGIVEESYTGVHRLYQLSKAGKLCVFAANVNDSVTKQKEDNLYCCRESILDGLKRTTD
VMFGGKQVVVCGYGEVGKGCCAALKALGAIVYITEIDPICALQACMDGFRVVKLNEVI
RQUDVVITCTGNKNVVTREHLLAMKNSCIVCNMGHSNYEIDVTSLRFPELTWERVRSQ
VDHYIMPDGKRVVLLAEGRLHLJSCSTVPTFVLSITATTQALALIELYNAPEGRYKQD
VYLLPKKMDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGFFKPNYYRY"

606 c 688 g 641 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        translation="MATVTKAPKKQIQFADDMQEFTKFPTKTGRRSLSRSISQSSTDS"
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1200	CCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGT	114: 116:	B &
1140 1162	TGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAAT 	110:	D Q
1080	TGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCA 	1021	g S
1020	GGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGAAGAGAGAG	961 983	B 8
960 982	TGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACT 	901 923	р Q
900	1 CAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTG	86	D Qy
840	1 CTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGGTTG	78 80	P 04
780 802	CCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTG		g S
720 742	GTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAAT	661	D Q
660	1 GACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAAC	60 62	B 8
600	1 APACCAACTCCAAGGGCAGCAGCAATTTCTGTGTGAAGAACATCAAGCAGGCAG	54	р Q
540 562	1 GTTCAGCTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGC	48 50	D 6
480 502	CCAAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCCTCACTGACAGCTACA	44 2	p Q
4 20 4 42	AGGCGCCCAAGAAGCAAATCCAGTTTGCTGATGACATGCAGGAGTTCACCAAATTCCCCA	36	P Q

FEATURES SOU	REMARK COMMENT	ACCESSION VERSION KEYWORDS SOURCE ORGANISN REFERENCE AUTHORS TITLE JOURNAL	Db 1823 RESULT 4 BC016942 LOCUS DEFINITION	2		
RES	ARK	,	ž	703 741 763	583	441 463 501 523
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINI at: http://image.llnl.gov Series: IRAK Plate: 20 Row: a Column: 15 This clone was selected for full length sequencing because it passed the following selection criteria: Similarity but not identity to protein. Location/Qualifiers 1. 2552 //db_xref="LocusID:10768" //db_xref="LocusID:10768" //clone="MGC:21453 IMAGE:3450568"	NIH-MGC Project URL: http://mgc.nci.nih.gov Contact: MGC help desk Emall: cgapbs-remail.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Library Preparation: Life Technologies, Inc. cDNA Sequencing by: Sequencing Group at the Stanford Human Genome Center, Stanford University School of Medicine, Stanford, CA 94305 Web site: Contact: (Dickson, Mark) mcd@paxil.stanford.edu Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers, R. M.	2.1 GI:1 Diens Diens La; Metaz R tuther	GACTCAACAAAATGGGCCATTCAAACCTAATTATTACAGATAC 1844			15 15 15

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368 301 308

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Query Match
Best Local Similarity
Matches 1836; Conser
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                                                                  GGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCA
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                                                       GGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCA
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AEAGVAVFAMKGESEDDFWGCIDRCVNNDGWQANMILDDGGDLTHWVYKKYPNVFKKI
RGIYBESVTGVHRLYQLSKAGKLCVPANNVNDSVTKQKFDNLYCCRESILDLKRFTD
VMFGGKQVVVCGYGEVGKGCCAALKALGAIVYITEIDPICALQACMDGFRVVKLNEVI
RQVDVVITCTONKNVVTREHLDRXKNSCIVCNNGHSNTEIDVTSLRTPELTWERVASQ
VDHVIMPDGKRVVLLAEGRLLNLSCSTVFTFVLSITATTQALALIELYNAPEGRYKQD
VYLLFKKMDEVVASLHLPSFDAHLTELTDDQAKYLGLIKNGPFKPNYRY"
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/clone_lib="NIH_MGC_10"
/lab_host="DH10B"
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This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, Similarity but not identity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hisiao, Martin Krzywinski, Reta Rutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Submitted (10-MAY-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                   · SES
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Contact: MGC help desk
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2526)
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VDHVIWPDGKRVVLLAEGRLLNLSCSTVPTFVLSITATTQALALIELXNAPEGRYKQD
                                                                                                                                                                                                        /translation="MATVIKAPKKQIQFADDMQEFIKFPIKIGRRSLSRSISQSSTDS
YSSAASYTDSSDDEYSPREKQQINSKGSSNECVKNIKQAEFGRRSEIEIAEQDMSALI
LRKRAQGEKELAGAKIYGCHHITAQTAVLIEFICALGAQCRMSACNIYSTONEVAALI
AEAGVAVFAWKGESEDDFWMCIDRCVNMDGWQANMILDDGGDLTHWVYKKYPNVFKKI
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                                                                                                                                                                                                                                                                                                                      'product="S-adenosylhomocysteine hydrolase-like 1"
'protein_id="AAH07576.1"
'db_xref="GI:14043177"
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'lab_host="DH10B-R"
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db_xref="LocusID:10768"
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                                                                                                    mRNA,
      Eukaryota; Metazoa; Chordata; Crani
Mammalia; Eutheria; Primates; Catar
1 (bases 1 to 2258)
Cleaver, J.E., Afzal, V., Feeney, L.,
Volpe, J.P.G., Busch, D.B., Coleman, F
Nagasawa, H.
                                                       Homo sapiens
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                                                                                                                       HSU82761
                                                                Homo sapiens.
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and Little, J.B.
                                                                                                              S-adenosyl
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      eeney,L., McDowell,M., Sadinski,W., Coleman,D.M., Ziffer,D:W., Yu,Y.,
                                  Craniata; Vertebrata; Catarrhini; Hominidae;
                                                                                                                       linear
                                                                                                             homolog
                                           Euteleostomi;
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                                                                                                             (XPVkona)
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Query Match
Best Local Similarity
Matches 1547; Conserv
                 TTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGĠA
                                                                                                      AGCTGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGGCCACCGTCA 357
TTGGACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGA
                                                                              ACAGTTCAGCTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGC
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2 (bases 1 to 2258)
7 (olpe, J. P. G., McDowell, M., Jostes, R. F., Afzal, V., Volpe, J. P. G., McDowell, M., Jostes, R. F., Afzal, V., Volpe, J. P. G., McDowell, M., Jostes, R. F., Afzal, V., Volpe, J. P., Complementation of chromosomal instability in the Complementation of chromosome on human chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (19-DEC-1996) 0750, San Francisco, CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Increased ultraviolet sensitivity and chromosomal increated to P53 function in the xeroderma pigmentosum Capoer Res. 59 (5), 1102-1108 (1999)
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YSSAASYTDSSDEVSPREKQQTNSKGSSNFCVKNIKQAEFGRREIEIAEQDMSALIS
LRKRAQGEKPLAGAKIYGCTHTAQTAVLIETLCALGAQCRWSACNIYSTQNEVAAAL
AEAGVAVFAWKGESEDDFWWCIDRCVMMDGWQAMMILDGGDITHWYKKYPNVFKKI
RGIVEESVTGVHRLYQLSKAGKLCVPAMNVNDSVTKQKFDNLYCCRESTLDGLKRTTD
VMFGGKQVVVCGYGEVGKGCCAALKALGAIVYITEIDPICALQACMDGFRVVKLNEVI
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VDHYIWPDGKRVYLLAEGRLLNLSCSTVPTFVLSITATTQALALIEL;VNAPEGRYKQD
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48. .1550
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/protein_id="AAC01960.1"
/db_xref="GI:2852125"
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/codon_start=1
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                                                                                                                      TGTCCATCACAGCCACACACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGG
                                                                                                                                                                         TCCTCCTGGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTC
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                                GGCGATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGCT
                                                                                                    TGTCCATCACAGCCACACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Clone distribution: MGC clone distribution information can be through the I.M.A.G.E. Consortium/LLML at: http://image.llnl.geries: IRAK Plate: 23 Row: n Collumn: 6
This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Glibert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu,
Yoon, V.S., Kowis, C.R., Lawrence,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (03-DEC-2001) National Institutes of Health Gene Collection (MGC), Cancer Genomics Office, Nation Institute, 31 Center Drive, Room 11A03, Bethesda, MD
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Contact: MGC help desk
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Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                     /lab_host="DH10B"
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	;AA 1111 . ;AA 957	2 CAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAG 	Qу 105 рь 89	
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	A 991 A 837	2 CCTGBATGATGGGGGAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAA 	Qy 93 Db 77	п о
	T 931	. m - H	Qy 87 Db 71	п о
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	% 511 % 357	32 GATCTCACAGTCCTCCACTGACAGCTACAGTTCAGCTGCATCCTACACAGATAGCTCTGI 	Qy 45 Db 29	п о
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	;A 391 A 237	32 GAAGTACTCCTTCATGGCCACCGTCACCAAGGCGCCCAAGAAGCAAATCCAGTTTGCTG 	Qy 33 Db 17	в о
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	GC 271 	2 AGGCGGGGGCGGGTCAGCCGCTGGCCGGCCGGGGGAATGTCGATGCCTGAC	Оу 21 рь 5	п о
	G 211 G 57	2 GGGCGATCGCGTGTCGGAGGGCGCCGCGCGCGCGCAGG 	Qу 15 Db	п о
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YRSQ YKQD	ELTWEF VAPEGF	RQVDVVITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVTSLRTPE VDHVIWPDGKRVVLLABGRLLMLSCSTVPTFVLSITATTQALALIELY VYLLPKKMDEYVASLHLPSFDAHLTELTDDQAKYLGLNKNGPFKPNYYI 462 a 406 c 506 g 398 t	BASE COU DRIGIN	OB

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JOURNAL Submits Martin	TITLE Direct Submission	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homb. EFERENCE 1 (bases 1 to 2510)	URCE Homo sapiens. ORGANISM Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E	CESSION ÂL049954 RSION AL049954 YWORDS	HSM8 HOMO HOMO	T 8		1832		1772 G		1712 6		1652 GATAGAACTCTATAATGCACCCGAGGGGGGGATACAAGCAGGATGTGTACTTGCTTCCTAA 17		1592 CTGCTCCACAGTTCCCACCTTTGTTCTGTCCATCACAGCCACAACACAGGCTTTGGCAC		b 1318 GACCAGCCTCCGCACTCCAGAAC	1472 GACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCGAGTACGTTCTCAGGTGGACC		1412 TCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACA	1198 GGTGGACGTTGTAATTACTTGCACAGGAAATAAGAATGTGAGTGA	1352 AGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATGTAGTGACACGGGAGCACTTGGA		1292 TGCTCTGCAGGCCTGCATGGATGGGTTCAGGGTGGTAAAGCTAAATGAAGTG		1232 CTGTGCTGCTCTCAAAGCTCTTGGAGCAATTGTCTACATTACCGAAATCGA	1018 TGTGATGTTTGGTGGGAAACAGGTGGTGGTGTGTGTGTGT	1172 TGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGCTATGGTGAGGTAGGCAAGGGG		1112
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                                                                            AAGATCTTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACAGTTCAGCTGCATC
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                                                                                                                                                 TGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGA
                                                                                                                                                                                                              GGGCAGCAATTTCTGTGAAGAACATCAAGCAGGCAGAATTTGGACGCCGGGAGAT 613
                                                                                                                                                                                                                                                                          AAGATCTTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACAGTTCAGCTGCATC 493
                                                                                                                                                                                                                                                                                                                                                                GCAAATCCAGTTTGCTGATGACATGCAGGAGTTCACCAAATTCCCCCACCAAAACTGGCCG
                                                                                                                                                                                                                                                                                                                                                                                sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing consortium of the German Genome Project.
This clone (DKFzp564A1523) is available at the RZPD in Berlin. Please contact the RZPD. Sis available at the RZPD in Berlin. Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at http://www.mips.biochem.mpg.de/proj/cDNA/.
                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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Query Mat Best Loca Matches]	BASE COUNT	CDS .	FEATURES Source		REMARK	SOURCE SOURCE ORGANISM REFERENCE RUTHORS TITLE JOURNAL	RESULT 9 BCO08349 LOCUS DEFINITION ACCESSION VERSION KEYFORDS
Query Match 54.2%; Score 999.2; DB 9; Length 2030; Best Local Similarity 75.1%; Pred. No. 1.8e-190; Matches 1279; Conservative 0; Mismatches 413; Indels 12; Gaps 2;	/protein_id="AAH03349.1" /db_xref="GI:1424936" /db_xref="GI:1424936" /translation="MSYQVVSAAAAAKYPEVELKDLSPSEAESQLGLSTAAVGAMAPP /translation="MSYQVVSAAAAAKYPEVELKDLSPSEAESQLGLSTAAVGAMAPP /GGGDPEAPAPARERPPVPGPGSGPAAALSPAAGKVPQASAMKRSDPHHQHQRHRDGG EALVSPDGTVTEAPRTVKKQIOPADKOEPKRFFVKIGRSLSRSISQSSTDSYSSAA SYTDSSDDETSPRDKQQKNSKGSSDFCVKNIKQAEFGRREIEIAPGEMPALMALRKRA QGEKPLAGAKIVGCTHITAQTAVLMETLGALGAQCRWAACNIXSTLNEVAAALAESGF PVFAWKGESEDDFWWCIDRCVVVEGWQPNMILDDGGDLTHWIXKKYPNMEKKIKGIVE ESVTGVHRLYQLSKAGKLCVPAMNVNDSYTKQKFPNLYCCRESILDGLKRTTDMMFGG KQVVVCGTGYGTGGCCAALKAMGSIVYTEIDPTCALQACMOGFRLYKLAWEVIRQVDI VITCTGNKNVVTREHLDRMKNSCIVCNMGHSNTEIDVASLRTPELTWERVRSQVDHVI WPDGKRLVLLABGRILMLSCSTVPTFVLSITATTQALALIELYNAPEGRYKQDVYLLP KKMDEYVASLHLPTFDAHLTELTDEQAKYLGLNKNGPFKPNYYRY" 539 a 492 c 548 g 451 t	/db_xref="taxon: 9066" /db_xref="taxon: 9066" /clone="IMAGE: 3536052" /tissue_type="Lung, small cell carcinoma" /clone_lib="NIH_MGC_7" /lab_host="9H10B-R" /note="Vector: pOTB7" <11838 /codon_start=3 /product="Similar to S-adenosylhomocysteine hydrolase-like	Clone throu Serie	CDMA Library Krepalecton: ROBLIN Habblacoty CDMA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Genome Sequence Centre, BC Cancer Agency, Vancouver, BC, Canada Info@bcgsc.bc.ca Info@bcgsc.bc.ca Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield, Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin, Letticia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo Sen Lee, Victor Ling, Carrile Mathewson, Candice McLeavy, Steven Ness, Pawan Pandoh, Anna-Liisa Prabhu, Parvaneh Saeedi, Jacqueline Schein, Duane Smailus, Michael Smith, Lorraine Spence, Jeff Stott, Michael Thorne, Miranada Tsai, Natasja van den Bosch, Jill Vardy, George Yang, Scott Zuyderduyn, Marco Marra.	ject URL: http://mgc. %C help desk %Ds-r@mail.nih.gov %urement: DCTD/DTP	Homo sapiens. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. 1 (bases 1 to 2030) Strausberg, R. Direct Submission Submitted (25-MAY-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,	BC008349 2030 bp mRNA linear PRI 12-JUL-2001 Homo sapiens, Similar to S-adenosylhomocysteine hydrolase-like 1, clone IMAGE:3536052, mRNA, partial cds. BC008349 BC008349.1 GI:14249935
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         NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human
Center, Stanford University School of Medicine, Stanford.
                                                                                                                                     Direct Submission
Submitted (01-MAR-2002) National Institutes of
Gene Collection (MGC), Cancer Genomics Office,
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BC024325.1 GI:19353091
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Series: IRAK Plate: 22 Row: 1 Column: 22
This clone was selected for full length seques passed the following selection criteria: Similarity to protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact:
Dickson,
R. M.
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/db_xref="GI:19353092"
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/clone_lib="NIH_MGC_71"
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/db_xref="LocusID:23382"
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  GGCTCTTGCCTTGATAGAGCTTTACAATGCTCCTGAGGGTCGCTATAAGCAGGATGTCTA
                                            GGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGCGATACAAGCAGGATGTGTA 1699
                                                                                          GCTGAACCTTAGCTGCTCCACAGTGCCTACATTTGTGCTCTCAATCACTGCTACTACTCA
                                                                                                               ACTCAATTTGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCCACCAGCCCACAACACA
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Homo sapiens mRNA for KIAA0828
AB020635
AB020635.1 GI:4240144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (02-DEC-1998) Osamu Ohara, Kazusa DNA Research Institute, Laboratory of DNA Technology; Yana 1532-3; Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913,
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Ohara,O., Suyama,M., Kikuno,R., Nagase,T.
Direct Submission
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GHQHHHDGGBALVSPDGTVTEAPRTVKKIQFADQKQENKRPKIGRRELSESISQSS
TDSYSSAASYTDSSDDETSPRDKQQKNSKGSSDFCVKNIQAEKIGRRELSEIIAEQEMPA
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AALAKRAQGEKPLAGAKIVGCTHIPAQTAVLMETLGALGAQCRMAACNIYSTLNEVA
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/db_xref="GI:4240145"
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/clone_lib="pBluescriptII SK
/dev_stage="adult"
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nome Center; Shi pan (E-mail:cdna	Shibahara, T., Tanaka, Shibahara, T., Tanaka, Direct Submission Submitted (29-AUG-20) University of Tokyo	NEDO human cDNA seque Unpublished 2 (bases 1 to 1987)	I (sites) 1 (sites) 1 (sites) Watanabe, K., Kumagai Ota, T., Suzuki, Y., O	clone: CCLF0094. Homo sapiens Eukaryota; Metazoa;	AKO25372.1 GI:104378 oligo capping; fis () Homo samiens colon mu	AK025372	GCCTAATTACTACAGGTA 185		TACAGAGATGACTATA	TGCCTTGATAGAGCTTTACAAT	CCTTAGCTGCTCCACAGTGCCT	CCATGTGATATGGCCTGATGGC			CTTGGATCGCATGAAAAACAGT	COGGCAAGTTGATGATATA	George General Service Control of the Control of th	AACAGACATGATGTTTGGTGGA
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ACTTGAAATTGACCC GCTAAATGAAGTCAC GCTAAATGAAGTCAC GCTAAATGAAGTCAC ATTAAATGAAGTCAT AGTGACACGGGAGCA	lalı 4-6-1, Minato-ku, Tokyo -tokyo.ac.jp, Tel:81-3-5449-	inio Sugano, Institute of Mec Catory of Genome Structure Ar	T., Obayashi,M., Nishi,T., I	Watanabe,K., Kumagai,A., Itakura,S., Yamazaki,M., Te Ota,T., Suzuki,Y., Obayashi,M., Nishi,T., Shibahara Nakamura,Y., Isogai,T. and Sugano,S. NEDO human CDNA sequencing project	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; ERENCE 1 (sites)	AK025372.1 GI:10437875 oligo capping; fis (full insert sequence). Homo sapiens colon mucosa cDNA to mRNA, clone_lib:Co clone:COLF0094. Homo sapiens	1987 bp mRNA linear P sapiens cDNA: FLJ21719 fis, clone COLF0094.	Db 1839 GCCTAATTACTACAGGTA 1856	Qy 1826 ACCTAATTATTACAGATA 1843	Qy 1766 TACAGAGCTGACAGATGACCAAGCAAAATATCTGGGGACTCAACAAAAATGGGCCATT	OY 1706 TCCTAAGAAAATGGATGAATACGTTGCCAGCTTGCATCTGCCATCATTTGATGCCCACCT	Qy 1646 GGCACTGATAGAACTCTATAATGCACCCGAGGGGGGATACAAGCAGGATGTGTACTTGCT	Qy 1586 TITGAGCTGCTCCACAGTTCCCACCTTTGTTCTGTCCATCACAGCCACAACACAGG¢T	QY 1526 CCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCTCCTGGCAGAGGGTCGTCTAC	OY 1466 CGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCGAGTACGTTCTCAGG	QY 1406 CTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTCCAACACAC 	a – a	Qy 1286 CATCTGTGCTCTGCAGGCCTGCATGGATGGGTTCAGGGTGGTAAAGCTAAATGAAG	Db 1239 AGGGTGCTGCTGCCCTGAAAGCCATGGGCTCCATTGTGTATGTA	acterior technique te transcription and the committee
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/clone_lib="Colf"
/note="cloning vector pME18SFL3"
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/db_xref="taxon:9606"
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Stapleton, M., Brokstein, P., Hong, L., Agbayani, A., Carlson, J., Stapleton, M., Chavez, C., Dorsett, V., Dresnek, D., Farfan, D., Frise, E., Ghampe, M., Chavez, C., Dorsett, V., Ronmiller, B., Li, P., Liao, G., George, R., Gonzalez, M., Guarin, H., Kronmiller, B., Li, P., Liao, G., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., Miranda, A., Mungall, C.J., Nunco, J., Pacleb, J., Paragas, V., Park, S., S., Rubin, G.M.
Direct Submission
Submitted (16-MAY-2002)
Lawrence Berkeley Nation
                                                                                                                                         Drosophila melanogaster.
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygot
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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Drosophila melanogaster RE58316
AY113501 GI:21064552
FLI_CDNA.
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full insert cDNA.
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                                         .00 .
ATTTCTGTGTGAAGAACATCAAGCAGGCAGAATTTGGACGCCGGGAAGATTGCAGATTGCAG
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AGGGTGCCAATATCGTCGGATGCACCCACGTCAATGCTCAGTCGGCAGTGCTGATCGAGA
                                                                                                                               AGCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGG
                                                                                                                                                                              ACTITITGCGTGAAGAGCATCTCGAAGAGTGCATTTGGAAGGCGGGAGATCGAGATCGCCG
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Sequence submitted by:
Berkeley Drosophila Genome
Lawrence Berkeley National
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VTGVHRLYMLSKGGKLTVPAIRVNDSVYKNKFDTFYTCRSLLDSLKRTTDIMFGGKQ
VVICCYGDVGKGCAQSLKGGGCIVYVTEVDPICALQAAMDGFRVVRLABVIRTYDVVY
TATGNKNVITRDHMNRMKNGCILCNMGHSCSEIDVNGLHTPELTWERVRSQVDHIRWP
DGRMIILLAEGRLVNLSCSTISSFVVSVASSTQALALLELFSAFGRYKSDVYLLPKKM
DEYVASLHLAIFDAHLTELTDEQKFWGLNKAGPFKANYYRY*

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/db_xref="01:21064553"
/db_xref="FLYBASE:FB9n0015011"
/db_xref="FLYBASE:FB9n0015011"
/translation="MAKMPETTFADLSLADKTAVKKSSIEARRESDVSTCSESSTCFT
GSSDEEDVSPKDNHQRNSAGGTDFCVKSISKSAFGRREIEIAESEMPGIMTLRKRAKD
EKPLKGANIVGCTHYVAAQSAVLIETLYQLGATYRWAACNIYSTQNAVAAALAEAGIPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-"alignment with genomic scaffold AE003715"
/db_xref-"FLYBASE:FBgn0015011"
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/strain="y; cn bw sp"
/db_xref="taxon:7227"
/map="89E10-89E10"
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Yu,W., Andersson,B., Worley,K.C., Muzny,D.M., Ding,Y., Liu,W. Ricafrente,J.Y., Wentland,M.A., Lennon,G. and Gibbs,R.A. Large-scale concatenation cDNA sequencing
Genome Res. 7 (4), 353-358 (1997)
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Andersson, B., Wentland, M.A., Ricafrente, J.Y., Liu, W. and Gibbs, R.A. a 'double adaptor' method for improved shotgun library construction a Note of the Construction and Construction (1996)
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PEGRYKQDVYLLPKKMDEYVASLHLPSFDAHLTELTDDQAKYLGLUKNGPFKPNYYRY
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                                                                                                     CDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium DNA Sequencing by: Institute for Systems Biology http://www.systemsbiology.org contact: amadan@systemsbiology.org Anup Madan, Rachel Dickhoff, Jessica Fahey, Stephan Greene, Mark Ketteman and Anuradha Madan
                  Clone distribution: MGC clone distribution through the I.M.A.G.E. Consortium/LLNL at: Series: IRAL Plate: 3 Row: b Column: 6.
                                                                                                                                                                                                                                                            Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: ht
Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                   Submitted (26-FEB-2001)
Gene Collection (MGC), C
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Location/Qualifiers
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Cancer Genomics Office, National
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/organism="Homo sapiens" /db_xref="taxon:9606"

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303 c 271 g 384 t
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Ttoh,M., Konno,H., Okazaki,Y., Muramatsu,N., and Hayashiraki,Y., Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genome Res. 10 (10), 1617-1630 (2000)
                                                                                                                                                                     Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303; 19-44 (1999)
99279253
                                                                                                                                                                                                                                                                                                                      HTC; CAP trapper.

Mus musculus (strain:C57BL/6J) 0 day neonate skin cDNA clone_lib:RIKEN full-length enriched mouse cDNA library.

clone:4631427C17.
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                                                                                                                                                                                                                                                                     Eukaryota; Metazoa;
Mammalia; Eutheria;
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BG6972|10 602660444
BE2707|73 600949331
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BG7747|19 602662763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Carninci, F., Fukuda, S., Fukunishi, Y., Furuno, M., Hanagaki, T., Hara, A., Hayatsu, N., Hill, D., Hiranoto, K., Hiraoka, T., Hori, F., Hume, D., Imotani, K., Ishil, Y., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okazaki, Y., Okido, T., Owa, C., Quackenbush, J., Saito, R., Sakai, C., Sakai, K., Sano, H., Sasaki, D., Schrimi, L., Shibata, K., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Shibata, Y., Tagawa, A., Takahashi, F., Tanaka, T., Tejima, Y., Toya, T., Yamamura, T., Yamanaka, I., Yasani, Shi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and
                                                                                                                                                                                                                                                                                                                                                                                  Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shibata,K., İtoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y., RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. cDNA went through one round of normalization to Rot = 10.0 and subtraction to Rot = 100.0. Second strand cDNA was prepared with the primer
                                                                                                               cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riker Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGGATCCAAGAGCTCTTTTTTTTTTTTVN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                       Pax:81-45-503-9216)
Papease visit our web site (http://genome.gsc.riken.go.jp/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Functional annotation of a full-length mouse cDNA collection Nature 409 (6821), 685-690 (2001)
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/clone_lib="RIKEN full-length enriched mouse
/dev_stage="0 day neonate"
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/strain="C57BL/6J"
/db_xref="FANTOM_DB:4631427C17"
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/db_xref="taxon:10090"
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74.8%;
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	1815 GGGCCATTCAAACCTAATTATTACAGA	δŌ
1855	1796 GATGCCCACCTGACAGAGCTAACAGATGAACAAGCCAAGTATCTGGGACTCAACAAG	밁
1814	1755 GATGCCCACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGGGACTCAACAAA	Ş
79	1736 GTGTACCTGCTACCCCAAGAAAATGGATATGTGGGCAAGCCTACACCTGC	물 5
1754	1695 GTGTACTTGCTTACTAAGAAAATGGATGAATACGTTGCCAGCTTGCATCTGCCATC	Ş
1694 1735	Y 1635 ACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGGGGG	B 5
1675	1616 CGTTTAATGAATCTCAGGTGCTCCACAGTGCCTACATTTGTGCTCTCCATCACTGCT	дb
1634	1575 CGTC	Q
61	1556 CCAATTTGATCATGTGATATGGCCTGATGGGCAAGAGGATAGTATTGCTGGCAGAGGGG	문
1574	1517 TCAGGTGGACCATGTCATCTGGCCAGAT-GGCAAACGAGTTGTCCTCCTGGCAGA-	Q
1555		밁
1516	1458 ACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCGAGTACG	Q
1495	b 1436 AGAGAGCACTIGGACCGTATGAAGAATAGCTGCATCGTTTGTAACATGGGCCATTCCAAC	D)
1457	1398 CGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCACTC	γQ
1435	1376 GAAGTCATCCGACAGGTCGACATTGTTATTACTTGCACAGGGAACAAGAATGTGGTAAC	망
1397	1338 GAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATGTAGT	δõ
1375	3 1316 ATTGACCCCATCTGTGCCCTGCAAGCCTGTATGGATGGAT	망
1337	1278 ATCGACCCCATCTGTGCTCTGCAGGCCTGCATGGATGGGTTCAGGGTGGTAAAGCTA	Qy
1315	DESCRIPTION OF THE PROPERTY OF	Д
1277	1218 GTAGGCAAGGGCTGCTGTGCTGCTCTCAAAGCTCTTGGAGCAATTGTCTACATTACCG	Qy
1255	1	뫄
1217	1158 AAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGCTATGGTG	Qγ
1195		망
1157	1098 GTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTGGATGGCC	γQ
<u> </u>	1076 CTGTACCACTGCAAAGCTGGGAAGCTGTGTGTTCCCGCCATGAACGTCAATGACTC	당 성
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1075		3 5
0	956 CAGCCAMACATGATACTGGATGATGGAGGAGATCTGACTCACTGGATTTATAA	당
	vo	Qy
955	896 GAGAATCAGAAGATTTTGGTGGTGCATTGACAGATGCGTGAATGTGGAGGG	문 :
917	. 858 GGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTGTGAACATGGATGG	Q V
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BP 191 91006 EVRY cedex - France
Email: seqref@enoscope.cns.fr,
Location/Qualifiers
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Full-length cDNA libraries
Unpublished (2001)
Contact: Genoscope
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AL551097
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0D1066YM07"
/clone="CS0D1066YM07"
/clone="Lib="LII.NFL006_PL2"
/fissue_type="placenta"
/note="Vector: pcMvSpORT 6; Site_1: NotI; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pcMvSpORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371
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Full-length cDNA libraries and normalizati
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Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-*Organ: brain; Vector: pCMVSPORT 6; 1st strand.cDNA was primed with a Notr-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact: Feng Liang Life Technologies, a division of invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 301 610 8371 Email: fileng@lifetech.com URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://fulllength.invitrogen.com"
238 c 299 g 158.t
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/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="CSODB002YL22"
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Plate: LLAM12117 row
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                                                                                                                                                                                                                                                                                                                                                                           Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    National Institutes of Health,
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/tissue_type="retinoblastoma"
/lab_host="PH10B (phage-resitant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo
Average insert size 1.75 kb. Library constructed by
                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5493677"
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QY 368 CAAGAAGCAAATCCAGTTTGCTGATGACAIGCAGGAGTTCACCAAATTCCCCACCAAAAC 427	Oy 308 GGCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGGCCACCGTCACCAAGGCGCC 367	Qy 248 CGGGGAATGTCGATGCCTGACGCGATGCCGCTGCCCGGGGTCGGGGAGGAGCTGAAGCA 307	Qy 188 CGGGCGGGCGCCAGAGGGGGAAAGAGGCGGGGGGGGGG	Qy 128 CGACGCAGGGGCCGGCAGGAGGGTGGGCGATCGCGTGTCCGAGGGCCCCCCGCGCGCAGG 187	QY 68 TGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCAGAAGCCGACGCAGCT 127	Qy 8 GCAGGTCGGAGCTGCAGCTGCTTCTGTTGTGGGCCACCGTCGCTGTCCGGC 67	Query Match 46.4%; Score 856.2; DB 9; Length 865; Best Local Similarity 99.2%; Pred. No. 2.2e-206; Matches 858; Conservative 2; Mismatches 5; Indels 0; Gaps 0;	/CLORE_TGSOUBNOVATION /CLORE_TGSOUBNOVATION /CLORE_TGSOUBNOVATION /CLORE_TGSOUBNOVATION /CLORE_TGSOUBNOVATION /CLORE_TGSOUBNOVATION /SEX="MILE" /tissue_type="neuroblastoma cells" /tissue_type="neuroblastoma cells" /lab_host="DH10B" /note="norgan: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6. vector. Library was commalized. Library was constructed vector. Library was constructed by Life Technologies. Contact: reng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax: (1) 8371 Email: filang@lifetech.com URL: http://fulllength.lnvitrogen.com" BASE COUNT 193 a 231 c 284 g 155 t 2 others	Location/Qualifiers 1. 865 /organism="Homo sapiens"	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. REFERENCE 1 (bases 1 to 865) AUTHORS LLW.B., Gruber, C., Jessee, J. and Polayes, D. TITLE Full-length cDNA libraries and normalization JURNAL Unpublished (2001) COMMENT Cencscope Genoscope - Centre National de Sequencage Bp 191 9106 EVRY cedex - France Emmall: secreferencecope cons fr. Web : www.genoscope.cns fr.	GI:12783064	RESULT 6 AL519571 AL5

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Plate: LLAM12332 row: m column:
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                    Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
                                                                                                                                                                                                                                                           Contact: Robert Strausberg, Ph.D.
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
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/clone_1ib="NIH_MGC_72"
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/tissue_type="melanotic melanoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: No: Site_2: Sall; Cloned unidirectionally. Primer: Olic Site_2: sall; Cloned unidirectionally. Primer: Olic Average insert size 2 kb. Library constructed by J Technologies."
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BM452485 BM452485.1 GI:18501525
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11 (bases 1 to 1042)
11 (hgc.)/mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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Location/Qualifiers
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    /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5493438"
/clone=lib="NHLMGC_67"
/clone="INHLMGC_67"
/tissue_type="retinoblastoma"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: Not1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.75 kb. Library constructed by Life
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Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www
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Li, W.B., Gruber
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end
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/lab_host="DH10B"
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/clone_lib="LTI_NFL003_NBC3"
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/db_xref="taxon:9606"
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                                                                                                CCGAGAAGTACTCCTTCATGGCCACCGTCACCAAGGCGCCCAAGAAGCAAATCCAGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC/DCTD/DTP
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov. 1 column: 20
High quality sequence stop: 670.
Location/Qualifiers
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AGENCOURT_6402958 NIH_MGC_72
5', mRNA sequence.
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National Institutes of Health, Mammalian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1999
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//tissue_type="melanotic melanoma"
/lab_host="PH010 (phage=resistant)"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1:
Site_2: Sall; Cloned unidirectionally. Primer:
Average insert size 2 kb. Library constructed
Technologies."
201 c 241 g 202 t 1 others
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/db_xref="taxon:9606"
/clone="IMAGE:5528995"
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97.7%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Ho
E 1 (bases 1 to 871)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectio
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI
Toshiyuki and Piero Carninci (RIKEN)
                                                                                                                                                                                                                                                                                                                                                                   AGAAG-TTTGATAACTTGTACTGCTGCCGAGAATCC--ATTTTGGATGGCCTGAAGAGĠA
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AGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCTCCTGGC
                                                                   CCACTCCAACACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        238
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/lab_host="DH10B"
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TCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCAGAAGCCGAC 120
                                       TCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCAGAAGCCGAC 121
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                                                                                                                                                           825;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can

found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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National Institutes of Health, Mammalian
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Mammalia; Eutheria;
1 (bases 1 to 928)
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Plate: LLCM2528 row: c column:
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                                                                                                                                                                                                                                                     /Clone_lib="NIH_MGC_43"
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/lab_host="DH10B (phage-resistant)"
/lab_host="DH10B (phage-resistant)"
/note="Organ: eye; Vector: pOTB7; Site_1: xhoI;
ECORI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC Library. |"
01 a 252 c 313 g 162 t
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/db_xref="taxon:9606"
/clone="IMAGE:6305605"
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections
                                                                                                                                                         mRNA sequence.
BI668412
BI668412.1 GI:15582645
           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkov
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  ment: Miklos Palkovits,
Preparation: Michael J.
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CDNA Library Arrayed by: The I.M.A.G. E. Consortium (LLN
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2563 BP; 646 A; 604 C; 677 G; 636 T; 0 other;
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Matches 1842
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(f) assessing the pro
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(h) assessing the agg
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25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
13-DEC-2000;
                                                                                                                                                                                                                                                                                                                                                                                 The invention relates to an isolated nucleic acid molecule (I) com a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
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131
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                                                                                                                                                                                                                                                                                                                                   ) assessing the efficacy of a therapy for inhibiting prostate cancer a patient;
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                                                                                                                                                                                                                                                               selecting a composition for inhibiting prostate cancer in a patien assessing the prostate cell carcinogenic potential of a compound; determining whether prostate cancer has metastasized in a patient, assessing the aggressiveness or indolence of prostate cancer in a
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The invention relates to an isolated nucleic acid molecule (I) com a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement. (I) asful for:

(a) assessing whether a patient is afflicted with prostate cancer;

(b) monitoring the progression of prostate cancer in a patient;

(c) assessing the efficacy of a test compound to inhibit prostate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer in a patient;
(d) assessing the efficacy of a therapy
in a patient;
(e) selecting a composition for inhibiti
(f) assessing the prostate cell carcinog
(g) determining whether prostate cancer
(h) assessing the aggressiveness or indo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel isolated nucleic acid molecule associated with cancerous sprostate cells and correlating with presence of prostate cancer, for detecting presence of prostate cancer, stage of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patient;
(I) is also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 6147-6148; 11750pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         selecting a composition for inhibiting prostate cancer in a passessing the prostate cell carcinogenic potential of a compodetermining whether prostate cancer has metastastzed in a pat assessing the aggressiveness or indolence of prostate cancer
                                                                                                                                                                                                                                                              GGCGCGGCAGGTCGGAGCTCGGAGCTGCTTCTGGTTCTCTTGTGGCCACCGTCCCT
                                                                            GTTCAGCTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGC
                                                                                                                                              CCAAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACA
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1842; Conserv
                               CCAAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACA
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           This sequence encodes a human S-adenosyl-5-homocysteine hydrolase (SAHH).

The SAHH protein can be used to generate specific antibodies and in drug compared to identify specific binding agents. Antagonists of the protein are used to treat or prevent a wide range of viral bacterial, compared parasitic, protozoal or helminthic infections, many cancers (cleukaemia, lymphoma or solid tumours), and many autoimmune diseases (e.g. acquired immune deficiency syndrome, allergy, asthma, diabetes mellitus, multiple sclerosis etc). All these conditions may be treated by carpressing antisense sequences, triplex-forming agents or ribozymes (cleroted against the nucleic acid. The nucleic acid and its fragments can be used as probes or primers for detecting and quantifying gene (compression, for diagnosis or monitoring of disease, to identify genetic variations, mutations or polymorphisms, in gene mapping and as antisense cutherapeutics. Antibodies are used directly as antagonists, indirectly to diseases in standard immunoassays, in competitive drug screens and to
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746
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                                                                                                                                                                                                                                                                                                                                                                                           TCGCTCGATCTCACAGTCCTCCACTGACAGCTACAGTTCAGCTGCATCCTACACAGATAG 505
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ACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAA 805
                                                                                                                                                   GCAAGACATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGC 685
                                                                                                                                                                                                                                                           CTTCTGTGTTAAGAACATCAAACAGGCAGAGTTTGGACGAAGAGAAATTGAAATTGCTGA 4393
                                                                                                                                                                                                                                                                                      TTTCTGTGTGAAAAAAAAACAGCAAGCAAGATTTGGACGCCGGGAGATTGAGAATTGCAGA 625
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                                                 TGGAGCCAAAATCGTGGGTTGCACACACACACTGCTCAGACTGCTGTGCTTATGGAAAC 4273
                                                                                 TGCTGACCAGAAGCAAGTTCAACAAACGTCCCACCAAAATTGGACGTCGCTCTTTGTC
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Pred. No. 1.8e-243;
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. 1822	1762 3252	1703 3312	1643 3372	1584 3432	1524 3492	1465 3552	1405 3612	1346 3672	1286 3732	1226 3792	1166 3852	1106 3912	1046 3972	986 . 4032	926 4092	866 4152	806 4212	4272
TCAAACCTAATTATTACAGATA 1843	2 ACCTTACAGAGCTGACAGATGACCAAGCAAAATATCTGGGACTCAACAAAAATGGGCCAT 1821 	GCTTCCTAAGAAATGGATGAATACGTTGCCAGCTT-GCATCTGCCATCATTTGATGCCC 1761 	TTTGGCACTGATAGAACTCTATAATGCACCCGAGGGGCGATACAAGCAGGATGTGTACTT 1702 	AATTTGAGGTGCTCCACAGTTGCCACCCTTTGTTCTGTCCATCACAGGCACAACAC-AGGC 1642 	GACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCTCCTGGCAGAGGGTCGTCTACTC 1583	TCGATGTGACCAGCCTCCGCACTCCGGAG-CTGACGTGGGAGCGAGTACGTTCTCAGGTG 1523	S ACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGGCCACTCCAACACAGAAA 1464 	S CCGGCAAG-TCGATGTCGTAATAACTTGCACAGGAAATAAGAATGTAGTGACACGGGAGC 1404 	S CATCTGTGCTCTGCAGGCCTGCATGGATGGGTTCAGGGTGGTAAAGCTAAATGAAGTCAT 1345 	GGGCTGCTGTGCTGCTCTAAAGCTCTTGGAGCAATTGTCTACATTACCGAAATCGACCC 1285	S CACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGGCTATGGTGAGGTAGGCAA 1225 	S ACAGAAGTITGATAACTIGTACIGCTGCCGAGAATCCATITTGGATGGCCTGAAGAGGAC 1165 	GETETECAAAGETGGGAAGETETGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAA 1105 	GTTTAAGAAGATCCGAGGCATTGTGGAAGAGAGCGTGACTGGTGTTCACAGGCTGTATCA 1045	CATGATCCTGGATGATGGGGGAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGT 985	AGAAGATGACTTCTGGTGGTGTATTGACCGCTGTGTGAACATGGATGG	TGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTC 865	

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                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               numan; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antilifective; gynaecologic; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
                                                                                                                                                                                                                                                                                                               cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polynucleotides may be used for detection of prostate cancer chromosome identification, as chromosome markers, and for numerous other diagnostic or research purposes. The prostate cancer antigens may be used to treat disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmopary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAF15566 to AAF16505 encode the human prostate cancer associated proteins, called prostate cancer antigens, given in AAB56363 to AAB57302 The prostate cancer antigens can have neuroprotective, cytostatic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF16004 standard;
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                                                                                                                                                                                                                                                            Sequence 721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       disorders such as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-MAR-2000;
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hes 703;
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                                                           61
                                                                                                                    1 GGCGCGGCAGGTCGGAGCTCGGAGCTGCTTCTGGTTCTCTTGTGGCCACCGTCGCT 60
                                      GTCCGGCTTGCGTTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCAGAAGCCGA 120
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DB; AAB56801.
                    GTCCGGCTGCCTTGGGCTGCCGAACAGACAAGGCGTGGGCCACAGCACCTCAGAAGCCGA
                                                                                                 GGCGCGGRCAGGTCGGAGCTCGGAGCTGCTTCTGGTTCTCTTGTGGCCGCCGTCGCT
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ROSEN C A.
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                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                            BP;
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Pred. No. 1.3e
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                                                                                                                                                                                                                                                          G; 119 T; 7 other;
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                                      WPI; 2001-656860/75
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  New isolated
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                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster
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reagent

for

detecting

1000 g

more

Claim

SEQ

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NO 5561;

genes from Drosophila and interactions -

Matches

Conservative

Query Match 37.6%; Best Local Similarity 70.4%;

Sequence 1566 BP;

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The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL01816)-ABL16175) and the encoded proteins (ABL01870-ABL16175) and the encoded proteins (ABB57737-ABB72072).
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New isolated nucleic a genes from Drosophila

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capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABLIG176-ABL30511), expressed DNA sequences (ABLIG176-ABL30511), expressed DNA (ABB37737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1776 BP; 437 A; 432 C; 479 G; 428 T; 0 other;
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                                                                                      CACTCTGTGCCCTGGGGGCTCAGTGCCTGGTCTGCTTGTAACATCTACTCAACTCAGA
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genes from Drosophila and
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Pred. No. 2.1e-119;
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The present invention describes a composition (I) comprising: and immunostimulants; and a polypeptide (II) of a ovarian tunn polypeptide encoded by a polypucleotide (III) having a cDNA se (S1) from the 10912 nucleotide sequences as given in ABL77023
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Composition for therapy and diagnosis of ovarian cancer comprising polypeptide of a ovarian tumor polypeptide, polynucleotide encoding polypeptide, antibody specific to polypeptide or T cell expressing polypeptide
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                                                                                                                                                                                                                                                                                                26-MAY-2000; 2000US-207484P
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CC (population of (II), or antigen presenting cells that express (II).
CC (I) has cytostatic activity. An oligonucleotide (IV) that hybridises to
CC (S1) can be used for detecting ovarian cancer in a patient's biological
CC sample preferably serum or ovarian tissue. The method comprises
CC contacting a biological sample from a patient with (IV), detecting the
CC amount of polynucleotide hybridising to (IV) and comparing the amount to
CC a predetermined cutoff value and thereby detecting ovarian cancer in the
CC contacting the amount of polynucleotide hybridising to (IV) is
CC detected preferably by polymerase chain reaction (PCR). (I) comprising
CC (III) and/or (II) is useful for stimulating and/or expanding T cells
CC specific for an ovarian tumour protein comprising contacting T cells
CC with (III) or (II). (III) is useful in design and preparation of
CC with (III) or (II). (III) is useful in design and preparation of
CC and proteins in tumour cells; and to isolate a full length gene from a
CC suitable library e.g., a tumour CDNA library using well known
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Matches 510; Conserv
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GACTCAACAAAA - - TGGGCCATTCAACCTAATTATTACAGATAC
                                                                         ATCTGCCATCATTTGNTGCCCACCTTACAGAGCTGACAGATGNCCAAGC-AAATATCTGG
                                                                                                                                                  ATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAATTGGATGAATACGTTGCCAGCTTGC
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RESULT 11 ABV44141/c

36

ABV44141 standard;

CDNA;

504

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EXXEXEXEX XX

16-SEP-2002

(first

entry)

Human; prostate cancer; pharmacogenomic marker;

cytostatic; carcinogen;

pharmacodyanamic

202

gene;

Human prostate expression marker cDNA 44132.

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Best Local S
Matches 422
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16-MAR-2000;
25-MAY-2000;
09-JUN-2000;
18-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      specification or its complement. (1) is useful for:
(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) assessing the efficacy of a therapy prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                            1006
                                                                                                                                                                                                                                                                                                                                                                                                            patient;
(I) is also useful as a pharmacodyanamic or pharmacogenomic marker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid molecule (I) comprising a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detecting presence of prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 8770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Schlegel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-662795/76
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                                                                                                                                                                                                                                                                                                                                           Local Similarity
nes 422; Conserv
AGTGCCGCTGGTCTGCTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGG 825
                                                                                                                                                                                                                                                                                 GAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCA
                                                                                                                            GTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGG
                                                                                                                                                                                  CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGGCGAGTCAGAAGATGACTTCTGGTGGT 885
                                                                                                                                                                                                                                                                                                             GTACACACATCACAGCCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCCTGGGGGGCTC 765
                                                     GAGACTTAACCCACTGGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCA.
                                                                                                            GTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGG
                                                                                                                                                                   CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGT
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; 2000US-189862P.
; 2000US-207454P.
; 2000US-211314P.
; 2000US-219007P.
; 2000US-255281P.
                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                         Score 422; DB
;; Pred. No. 1.1
0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                       1.1e-102;
                                                                                                                                                                                                                                                                                                                                                                       DB 23;
                                                                                                                                                                                                                                                                                                                                                                    Length 504;
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RESULT 12
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Best Local Similarity
Matches 852; Conserv
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                                                                                                                                                                                                                                                                                    capable of detecting 1000 or more genes from Drosophila. The invention useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (ABB57737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                                                     New isolated nucleic acid
genes from Drosophila and
interactions -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 23-MAR-2001; 2001WO-US09231.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pharmaceutical;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster genomic polynucleotide SEQ
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                                                                                           2826
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; SEQ ID NO 40831; 21pp + Sequence Listing; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Venter JC,
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11-JUL-2000;
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                                                                                                                                                                                                              Sequence 5537
                                                                                                                                                                                                                                                          The sequence data specification, but
                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to an isolated nucleic acid detection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (PEKE ) PE
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                                                                                                                                                                                                                                       e sequence data for this patent did not form part of the printed ecification, but was obtained in electronic format directly from ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TCTTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACAGTTCAGCTGCATCCTAC 497
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                               GGAAGCTCCGACGAGGAAGACGTCTCCCCGAAGGACAACCATCAGCGCAACTCCGCCGGA
                                                         ACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGCAAACCAACTCCAAGGGC
   AGCAGCAATTTCTGTGTGAAGAACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGAG
                                                                                          TCTCTTTGCGATTGAACTCACTTAATGGTCACTTGATCTCTTTGTTAGCCTGTTTCACC
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2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  detection reagent for detecting for elucidating cell signalling
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                                                                                                                                                                 Score 421.6; DB 23;
Pred. No. 4.4e-102;
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                                                                                                                                                                                  ATGTAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGG
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                  AGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAGTTGTCCTCC
                                                                                                           GACATTCCTGCTCGGAGATTGATGTGGTATGTATTCGGGGGTGATTCCATTGTGGCCTTCA
                                                                                                                                       GCCACTCCAACACAGAAATCGATGT-----
                                                                                                                                                                                                                                             TAAAGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGA 1386
                                                                                                                                                                                                                                                                                         GGTACGGTGATGTGGGAAAGGGCTGTGCCCAGTCCCTGAAGGGCCCAAGGATGCATTGTTT
                                                                                                                                                                                                                                                                                                                                                                    GCTATGGTGAGGTAGGCAAGGGCTGCTGCTGGCTCTCAAAGCTCTTGGAGCAATTGTCT
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                                              TATATCAAAAGGTTTTTAACCCACTTTAGAATGGCTTGCATACCCCGGAGCTAACGT¢GG
                                                                                                                                                                                                                               TACGGCTCAACGAGGTCATCAGGACGGTGGATGTGGTGGTTACGGCAACTGGAAACAAAA
                                                                                                                                                                   ATGTTATTACCAGGGATCACATGAATCGCATGAAGAATGGTTGTATCCTCTGCAATATGG
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3425

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1206

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857 3185 797

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-GACCAGCCTCCGCACTCCGGAGCTGACGTGGG

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ID AAZ807
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                                             Query Match
Best Local Similarity
Matches 418; Conserv
                                                                                                                        AAZ79917 to AAZ80766 represent double stranded cDNA clones isolated from the human colorectal adenocarcinoma (colon cancer) cell line SW480. The cDNA clones can be used to generate antisense oligonucleotides which can be used for antisense therapy. Methods and products from the present invention can be used for identifying and/or classifying cancerous cells present in a human tumour, particularly in solid tumours, e.g. carcinomas and sarcomas, e.g. breast or colon cancers. The CDNA clones can be used for developing agents for the diagnosis and treatment of disorders involving unwanted cell proliferation, such as neoplasia, dysplasia or hyperplasia.
                                                                                                                                                                                                                                                                                                                                                                                                                   Endege WO,
Carroll E,
Schlegel R;
                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                  Claim 15;
                                                                                                                                                                                                                                                                                                                          Novel nucleic acids, used to develop products ; treatment of disorders involving unwanted cell particularly cancers, especially colon cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4203
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                colorectal adenocarcinoma; cytostatic; sarcoma; breast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human colon
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          707 TACACACATCACAGCCCAGACAGC-GGTGTTGATTGAGACACTCTGTGCCCCTGGGGGGCTC 765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hyperplasia;
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2000-087220/07
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene expression product; diagnosis; tumour; colon cancer;
ctal adenocarcinoma; cell line SW480; cell proliferation;
atic; sarcoma; breast cancer; neoplasia; dysplasia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BAYER CORP
                                                                                                         636
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                                                                                                                                                                                                                                                                                             Page 469; 469pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                               Steinmann R
Catino TJ,
                                             Conservative
                                                                                                       BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer cell line SW480 cDNA clone SEQ ID NO:850
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                                                                                                    156 A; 166 C; 137 G;
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                                                          22.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                               KE, Astle JH, Burg
, Derti A, Ford DM,
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                                                          Score 406.4;
Pred. No. 1.8
                                            Pred. No. 1.8
); Mismatches
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                                                                                                   147 T; 30 other;
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d DM, Lewis
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                                                  Claim 1;
                                                                      Novel isolated nucleic acids comprising sequences encoding useful for treating or diagnosing e.g. cancer
                                                                                                                                                                                                                                                                                                                                                 antiinflammatory; antithyroid; antiallergic; antibacterial; cardiant; dermatological; neuroprotective; thrombolytic; coagulant; nootropic; vasotropic; antipaoriatic; antiangiogenic; gene therapy; inflammation; immune disorder; haematopoietic cell disorder; autoimmune disorder; allergic reaction; graft versus host disease; organ rejection; haemostatic; thrombolytic; cardiovascular disorder; infection; neurological disease; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; cancer associated gene; cancer antigen; detection; cancer; diagnosis; cytostatto; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antipiral;
                                                                                                                                                                                                                                         08-MAR-2000;
                                                                                                                    P-PSDB; AAB43614.
                                                                                                                                                                                                                12-MAR-1999;
                                                                                                                                                                                                                                                                     21-SEP-2000
                                                                                                                                                            Rosen CA,
                                                                                                                                                                                      ( HUMA - )
                                                                                                                                                                                                                                                                                             WO200055350-A1
                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human cancer associated gene sequence SEQ
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                                                                                                                                                                                     HUMAN GENOME
                                                  Page 787-788;
                                                                                                                                                          Ruben SM
                                                                                                                                                                                                                                         2000WO-US05882
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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AAC77607 to AAC78448 encode the human cancer associated proteins in AAB43398 to AAB44239. The proteins can have activities based tissues and cells the genes are expressed in. Example of activit.

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Best Local S
Matches 741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           polynucleotides, polypeptides, antibodies, agonists and antagonists from the present invention may be used to treat immune disorders by activating or inhibiting the proliferation, differentiation or mobilisation of immune cells, to treat disorders of haematopoietic cells, autoimmune disorders, allergic reactions, graft versus host disease and organ rejection, modulate haemostatic or thrombolytic activity, modulate inflammation, cancers, cardiovascular disorders, neurological disease and bacterial or viral infections. The peptides, nucleotides, antibodies, agonists and antagonists may be also be used in drug screens. AAC78449 to AAC78457 and AAB44240 represent sequences used in the exemplification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   include: cytostatic; proliferative; vulnerary; immunomodulator; antidiabetic; antiasthmatic; antirheumatic; antiarthritic; antiinflammatory; antithyroid; antiallergic; antibacterial; antiviral; dermatological; neuroprotective; cardiant; thrombolytic; coagulant; nootropic; vasotropic; antipsoriatic and antianglogenic. The polynucleotides and polypeptides can be used for preventing, treating or ameliorating medical conditions and diagnosing pathological conditions.
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                                                                                                                                   ACTTGTACTGCTGCCGAGAATCCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGT
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CCCTGCGGGGTTTCGGAGCCCGCGTCATCATCACCGAGATTGACCCCATCAACGCACTGC
                                                                                     TIGGTGGGAAACAAGIGGTGTGTGTGTGGCTATGGTGAGGCAAGGGCTGCTGTGCTG
                                                                                                                                                                                                           GGATCCTCAAGGTGCCTGCCATCAATGTCAATGACTCCGTCACCAAGAGCAAGTTTGACA
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                                CTCTCAAAGCTCTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGC
                                                                     TTGCCGGCAAGGTAGCGGTGGTAGCAGGCTATGGTGATGTGGGCAAGGGCTGTGCCCAGG
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16-MAR-2000; 2000US-189862P.
25-MAY-2000; 2000US-217314P.
09-JUN-2000; 2000US-211314P.
18-JUL-2000; 2000US-219007P.
13-DEC-2000; 2000US-255281P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cancer in a patient;
(d) assessing the efficacy of a therapy for inhibiting prostate cancer in a patient;
(e) selecting a composition for inhibiting prostate cancer in a patient;
(f) assessing the prostate cell carcinogenic potential of a compound;
(g) determining whether prostate cancer has metastasized in a patient;
(h) assessing the aggressiveness or indolence of prostate cancer in a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to an isolated nucleic acid molecule (I) com a nucleotide sequence given in Tables 1-9 (ABV00010-ABV62213) of t specification or its complement (I) is useful for:

(a) assessing whether a patient is afflicted with prostate cancer;
(b) monitoring the progression of prostate cancer in a patient;
(c) assessing the efficacy of a test compound to inhibit prostate
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                                                                                                                                                                                                                                                                                                  1000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel isolated nucleic acid molecule associated with cancerous state of prostate cells and correlating with presence of prostate cancer, useful for detacting presence of prostate cancer.
                                                                                                                                                                                                                                                                                                                                                                                   940
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 detecting presence of prostate cancer, stage of prostate cancer
TTGGTGGGAAACAAGTGGTGGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGCTG
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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APPLICANT: Lewis, Marcia E.

APPLICANT: Monahan, John E.

APPLICANT: Monahan, John E.

APPLICANT: Schlegel, Robert

TITLE OF INVENTION: NOVEL HUMAN GENES AND GENES FILE REFERENCE: CCD-257 (US)

CURRENT APPLICATION NUMBER: US/09/328,111

CURRENT APPLICATION NUMBER: US/09/328,111

CURRENT FILING DATE: 1999-06-08

EARLIER APPLICATION NUMBER: US 60/088,801

EARLIER FILING DATE: 1998-06-10

NUMBER OF SEQ ID NOS: 850

SEQ ID NO 850

LENGTH: 636

TYPE: DNA

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                CTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGCCGAGTCAGAAGATGACTTCTGGTGGT
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US-07-885-971-15
US-08-194-0889-15
US-08-194-087-15
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US-09-165-2648-15
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US-09-130-145-568A-11
US-08-90-3800A-3
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April 20, 2003, 23:48:04;

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Sequence 26, Application US/09318448
Patent No. 6210950
GENERAL INFORMATION:
APPLICANT: Johnson, William G.
APPLICANT: Stenroos, Edward S.
TITLE OF INVENTION: METHODS FOR DIAGNOSING, PRILE REFERENCE: 601-1-057
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CURRENT FILING DATE: 1999-05-25
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 26
LENGTH: 2211
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Best Local Similarity
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Pred. No. 1.2e-72;
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US-09-347-878-2
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CURRENT FILING DATE: 1999-07-06
NUMBER OF SEQ ID NOS: 75
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 2
LENGTH: 2211
TYPE: DNA
ORGANISM: Homo sapiens
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Matches 498; Conservative
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                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Human S-adenosylhomocysteine hydrolase cDNA PUBLICATION INFORMATION: DATABASE ACCESSION NUMBER: M61831/GenBank
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TITLE OF INVENTION: METHODS
FILE REFERENCE: 25885-1651
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CCATTGCCAAGGCTGCATTCCGGTGTATGCCTGGAAGGGCGAAACGGACGAGGAGTACC
                                                                        CTGGCTGCCTCACATGACCGTGGAGACGGCCGTCCTCATTGAGACCCTCGTCACCCTGG
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US-09-103-840A-1/c
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Best Local Similarity
Matches 499; Conserv
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SEQ ID NO 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 2436-20007.00 CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FILLING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2
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                                            3628976 TGCTGCGGCTCTACCAATTCGCCGCGGCGGCGGTCTGGCCTTCCCGGCGATCAACGTCA 3628917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGAAGCTCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATA 1119
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    ATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAATCCATTTTGG 1149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AGGCCTGCATGGATGGGTTCAGGGTGGTAAAAGCTAAATGAAGTCATCCGGCAAGTCGATG 1359
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                                                                                                                        ACAAGTGGACCAAGATAGCCGAGTCGGTCAAGGGCGTCACCGAGGAGACCACCACCGGCG 3628977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VENTER, John C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WHITE, Owen R. FRASER, Claire M.
                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                           12.8%;
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                                                                                                                                                                                                      Score 236.2; DB 4;
Pred. No. 9.2e-51;
0; Mismatches 373;
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                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application Patent No. 5910444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3628676 CCGTCGAGGAGGCCATCGGGGACGCCGACATCGTCGTCAACCGCGAACAAAGACA 3628617
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                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: MASUTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3628616 TCATCATGCTCGAGCACATTAAGGCGATGAAGGACCACGCGATCCTGGGAAATATCGGCC 3628557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3628496 TCAAGCCTCAGGTCGACCTGTGGACCTTTGGCGACACGGGCCGCTCGATCATCGTGCTGT 3628437
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3628556 ACTTCGACAACGAGATCGACATGGCCGGGCTGGAGCGCTCCGGGGGCGACACGGGTCAACG 3628497
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                                                                                                                                                                                         APPLICANT: KUWATA, SITITLE OF INVENTION: (TITLE OF INVENTION: (NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1684 ACAAGCAGGATGTGTACTTGCTTACTAAGAAAATGGATGAATACGTTGCCAGCTTGCATC 1743
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1567 CAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACC---TTTGTTCTGTCCA 1623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1390 TAGTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCC 1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1330 AGCTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATG 1389
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1804 TCAACAAAAATGGGCCATTCAAACCTAATTATTACAGATAC 1844
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1744 TGCCATCATTTGATGCCCACCTTACAGAGCTGACAGATGACCAAAGCAAAATATCTGGGAC 1803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1450 ACTCCAACACAGAAATCGATGTGACCAGCCTCCGCACTCCGGAGCTGACGTGGGAGCGAG 1509
                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                     STATE:
                                                                                                                             STREET:
                                                          COUNTRY:
                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                  UEHARA,
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ORGANISMS IN WHICH THE
S-ADENOSYLHOMOCYSTEINE
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LENGTH: 1812 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA to mRNA
US-08-669-536-1
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INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1812 base pairs
                                                                                                                                                                                                                                                                                                                             1452 TCCAACACAGAAATCGATGTGACCAGCCTCCGCAC---TCCGGAGCTGACGTGGGAGCGA 1508
                                                                                                                                                                                                                                                                                                                                                                                                                                  1392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1332 CTAAATGAAGTCATCCGGCAAGTCGATGTCGTAATAACTTGCACAGGAAATAAGAATGTA 1391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1032 CACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCATGAACGTCAAT 1091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: MURCHY JR, GERALD M
REGISTRATION NUMBER: 28,971
REFERENCE/DOCKET NUMBER: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
1623 ATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACC---CGAGGGG
                                                                                                                                                                            1174 ATTAAGCCTCAAACCGACAGATGGGTCTTCCCTGACACCAACAGTGGCATCATTGTCTTG
                                                                                                                                                                                                                                                                           1114 TTTQACAACGAAATCGACATGCTTGGTCTCGAGACCTACCCTGGTGTCAAGAGGATCACA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1152 GCCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAACAAGTGGTGGTGTGTGGCTAT 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      634 ANATATACCAAGATGAAGGANAGACTCGTCGGTGTTTCTGAGGAAACTACCACTGGAGTT 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     972 AAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGAAGAGAGCGTGACTGGTGTT 1031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      934
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        874 GGAGATGTCGGCAAGGGTTGTGCTGCTGCCTTGAAACAAGCCGGTGCCCGTGTGATTGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       y Match 12.1%;
Local Similarity 56.4%;
hes 499; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                               GTGACACGGGAGCACTTGGATCGCATGAAAAACAGTTGTATCGTATGCAATATGGGCCAC 1451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGTGAGGTAGGCAAGGGCTGCTGTGCTGCTCTCAAAGCTCTTGGAGCAATTGTCTACATT 1271
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                                                                                                    GCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCACC---TTTGTTCTGTCC
                                                                                                                                                                                                                         GTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGCAAACGAG---TTGTCCTCCTG
                                                                                                                                                                                                                                                                                                                                                                                ATCATGGTTGACCACATGAGGAAGATGAAGAACAATGCCATTGTTTGCAACATTGGTCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CTAGAGGATGTCGTTTCTGATGTTGATCTTTGTCACCACGACCGGTAACAAGGACATT 1053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACCGAGATTGACCCTATCTGTGCTCTCCAGGCTACCATGGAAGGCCTCCAGGTCCTTACT
                                                                          GCTGAGGGTCGTCTCATGAACTTGGGGATGTGCCACAGGACACCCTAGTTTTGTGATGTCG
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Pred. No. 1.1e-48;
0; Mismatches 374;
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                                                                                                                         ; OTHER INFORMATION: US-08-930-894-1
                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1,
Patent No. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9
FILING DATE: 10-APR-1995
INFORMATION FOR SEQ ID NO: 1
                                                                                                                                                                                                                   MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1414
                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 1767 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: LDVA
COMPUTER: MS WOID
OPERATING SYSTEM: P
OPERATE: MS WOID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1354 AAGTATGAGAAGAAAGTGTATGTCTTGCCAAAACACCTCGACGAGAAGGTTGCTGCACTT 1413
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1680 CGATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGCTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1294 TGCTCGTTCACTAACCAAGTCATTGCCCAACTCGAGTTGTGGAATGAAAAGAGCAGTGGG 1353
                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: S-ADENOSYL-L-HOMOCYSTEIN HYDROLASE NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                            596 AAGTACAGGAAGATGAAGGATAGGATTGTCGGTGTGTCGGAGGAGACCACCACCGGGGT¢
                                                                                                                                                     NAME/KEY:
                                                                     Local
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: PCT/CFILING DATE: 10-APR-1996
                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 20005-3918
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1100 New
CITY: Washington
                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                               STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
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                                                           494;
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                                                                         Similarity
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SKIPSEY, Marc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WARNER, Simon
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                                                           Conservative
                                                                                                                                                                                                                                                                                    linear
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                                                        Score 214.6; DB 3;
Pred. No. 1.3e-46;
0; Mismatches 379;
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US-08-896-005-2
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Patent No. 5854023
                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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                                                                                                                           APPLICANT: Hillman, Jennifer L.
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: STADENOSYL-L-HOMOCYSTEINE HYDROLASE
NUMBER OF SEQUENCES: 5
                                                                                                     CORRESPONDENCE ADDRESS
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                                                                               ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATCAAGCCCCAGACTGACCGGTGGGTCTTCCCTGAAACCAACACTGGTATAATTGTTCTT 1195
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                           Palo Alto
                                                    3174 Porter Drive
                                                                               Incyte Pharmaceuticals,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1375
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Query Match
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RESULT 8
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                                                                                                                                                                                                                   SEQ ID NO 3
LENGTH: 2226
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/09347878C Patent No. 6376210 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches 117;
                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/347,878C CURRENT FILING DATE: 1999-07-06 NUMBER OF SEQ ID NOS: 75 SOFTWARE: Patentin Ver. 2.0
                                               NAME/KEY: misc_feature LOCATION: (1)..(226)
OTHER INFORMATION: Polynucleotide encoding human OTHER INFORMATION: S-adenosyl-5-homocysteine hydrolase OTHER INFORMATION: from bladder; n-a, c, g, or t PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES FILE REFERENCE: 25885-1651
                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Yuan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
PATENT DOCUMENT NUMBER: 08/896,005
PATENT FILING DATE: 1997-07-17
PUBLICATION DATE: 1998-12-29
                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1788
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/8 FILING DATE: Filed Herewith PRIOR APPLICATION DATA:
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ZIP: 94304
COMPUTER READABLE FORM:
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ATTORNEY/AGENT INFORMATION:
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100.0%; Pred. No. 4.8e-21;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 289 bacc -
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TOPOLOGY: lin
MOLECULE TYPE:
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TITLE OF INVENTION: Methods for Identifying
TITLE OF INVENTION: Suppressor Elements and
TITLE OF INVENTION: Growth in Cancer Cells
NUMBER OF SEQUENCES: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: 312-715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                 135 GCCTGATGCGTATGCGGGAGCGGTACTCGGCCTCCAAGCCACTGAAGGGCGCCCCGCATCG 194
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ATTORNEY/AGENT INFORMATION:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Palana "1"
                                                                                                                                                                                                      Local Similarity
les 126; Conserva
                                                                                                                                                                                                                                                                                                                                 TYPE: nucleic acid
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CTGGCTGCCTGCACATGACCGTGGAGACGGCCGTCCTCATTGAGACCCTCGTCACCCTGG
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10 S. Wacker Drive, Suite 3000
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35,303
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                                                                                                                                                                                               Score 72.6; DB 1;
Pred. No. 7.9e-10;
0; Mismatches 89;
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; Mismatches 0;
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Best Local Similarity Do...
126; Conservative
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: U5/09/081,16
FILING DATE: 18-MAY-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6083745nan, Kevin E
REGISTRATION NUMBER: 35,303
REGISTRATION NUMBER: 35,303
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CITY: Chicago
TATE: Illinois
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
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    255
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                           760 GGGCTCAGTGCCGCTGGTCTGCTTATCATCTAC 794
                                                         195 CTGGCTGCCTGCACATGACCGTGGAGACGGCCGTCCTCATTGAGACCCTCGTCACCCTGG
                                                                                       135 GCCTGATGCGTATGCGGGAGCGGTACTCGGCCTCCAAGCCACTGAAGGGCGCCCCGCATCG
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GTGCTGAGGTGCAGTGCCAGCTGCAACATCTTC 289
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Suppressor Elements and
Growth in Cancer Cells
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Pred. No. 7.9e-10;
0; Mismatches 89;
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US-09-081-395-8
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Sequence 8, Application US/09416833 
Patent No. 6197521 
GENERAL INFORMATION: 
APPLICANT: Gudkov, Andrei
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: NO. 6083746nan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,
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TELEPHONE: 312-913-0001
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Similarity 58.6%;
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Pred. No. 7.9e-10;
0; M1smatches 89;
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Genes Associated with Malignant
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                                                                                                                       RESULT 13
                                                                        Sequence 8, Application PC/TUS9502521 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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TITLE OF INVENTION:
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APPLICATION NUMBER:
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STRANDEDNESS: single
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Suppressor Elements and
Growth in Cancer Cells
              Methods for Identifying Genetic
Suppressor Elements and Genes Associated
Growth in Cancer Cells
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Pred. No. 7.9e-10;
0; Mismatches 89;
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Hest Local Similarity 58.6%;
Matches 126; Conservation
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                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DDS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/204,740
FILING DATE: 04-MAR-1994
 REFERENCE/DOCKET NUMBER: 9: TELECOMMUNICATION INFORMATION TELEPHONE: 312-715-1000
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LENGTH: 289 base pairs
                                                                                   CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION:
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MEDIUM TYPE: Floppy disk
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REGISTRATION TONNET NUMBER: 93,354-C
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
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ZIP: 60606
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10 S. Wacker Drive, Suite 3000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 285 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                 CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6083745nan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93
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LENGTH: 285 base pairs
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ITLE OF INVENTION:
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3.7%;
Best Local Similarity 56.8%;
Matches 126; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    184 CGCATTGCTGGCTGCCTGCGCATGACCGTGGAGACTGCTGCTTCTCATTGAGACTCTCGTG 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  633 ATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCT 692
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300 S. Wacker Drive,
                                                                                                                                                                                                                                            Kazarov, Alexander
                             McDonnell Boehnen Hulbert & Berghoff
                                                                                                        Methods for Identifying
Suppressor Elements and
Growth in Cancer Cells
                                                                                                                                                                                            Igor B
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Pred. No. 9.9e-09;
0; Mismatches 96
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                                                                                                                                   Genes Associated with Malignant
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Page 9

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244 GCCTGGGTGCTGAGGCGCGGTCGTCCAGCTGCAACATCTTC 285	753 GCCCTGGGGGCTCAGTGCCGCTGGTCTGCTTGTAACATCTAC 794	184 CGCATTGCTGGCTGCCTGCGATGACCGTGGAGACTGCTGTTCTCATTGAGACTCTCGTG 243	693 AAAATAGTGGGCTGTACACAACATCACAGCCCAGACAGCGGTGTTGATTGA	124 ATGCCAGGGTTGATGCGCATGCGGGAGATGTACTCAGCCTCCAAGCCACTGAAGGGTGCT 183	633 ATGTCTGCTCTGATTTCACTCAGGAAACGTGCTCAGGGGGAGAAGCCCCTTGGCTGGTGCT 692	64 GTCGCGGACATCGGACTGGCCGCCTGGGACACGCTCTGGATATAGCTGAGAATGAG 123	573 GTGAAGAACATCAAGCAGGCAGAATTTGGACGCCGGGAGATTGAGATTGCAGAGCAAGAC 632	Query Match 3.7%; Score 68.4; DB 3; Length 285; Best Local Similarity 56.8%; Pred. No. 9.9e-09; Matches 126; Conservative 0; Mismatches 96; Indels 0; Gaps 0;	; STRANDEDNESS: single ; TOPOLOGY: linear ; MOLECULE TYPE: cDNA US-09-081-167a-6

Search completed: April 21, 2003, 05:16:14 Job time: 2569.43 secs

Run

OM nucleic -

Scoring table:

Perfect score:

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Total number of hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries
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      Published_Applications_NA: *
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/cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
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0 US-09-920-300A-1423
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0 US-09-880-107-346

0 US-09-759-990

US-09-738-626-836

US-09-746-660A-97
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Sequence 836, App
Sequence 97, Appl
Sequence 1, Appl
Sequence 101, App
Sequence 838, App
Sequence 26, Appl
Sequence 4, Appl
Sequence 4421, Ap
Sequence 1143, Ap
Sequence 1143, Ap
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e 439, App
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                                                                                                                                                                                                                           NAME/KEY: CDS

LOCATION: (3)..(1847)

OTHER INFORMATION: Open reading frame extends without a stop codon OTHER INFORMATION: for the full 5' nucleotide sequence. The OTHER INFORMATION: initiation codon has yet to be identified. US-09-782-051-1
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US-09-782-051-1
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Patent No. US20020035078A1
GENERAL INFORMATION:
APPLICANT: Hart, Derek N J
TITLE OF INVENTION: Enzyme having S-adenosyl-L-homocysteine hydrolase
TITLE OF INVENTION: (AHCY) type activity
FILE REFERENCE: 24305 MRB
CURRENT FILING DATE: 2001-02-14
PRIOR APPLICATION NUMBER: PCT/NE97/00133
PRIOR FILING DATE: 1997-10-06
PRIOR FILING DATE: 1997-10-06
PRIOR FILING DATE: 1997-10-06
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: NZ 299507
PRIOR FILING DATE: 1996-10-04
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 2563
                                                                                                                                                             Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 1844; Conservative 0;
                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
     121 CGCAGCTCGACGCAGGGGCCGGCAGGAGGGCTGGCGATCGCGTGTCGGAGGGCGCCGCGC
                                                              61
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136.
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124.
114.
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1108.
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US-09-960-352-1365
US-09-960-352-1365
US-09-960-352-7284
US-09-960-352-2551
US-09-960-352-2551
US-09-970-445-679
US-09-960-352-2035
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US-09-960-352-10555
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US-09-738-626-837
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US-09-998-598-2191
US-09-960-352-12928
US-09-960-352-7006
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US-09-770-149-117
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Pred. No. 0;
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                                                                                                                                                                                               Length 2563;
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Sequence 1179, Ap
Sequence 1179, Ap
Sequence 1179, Ap
Sequence 2191, Ap
Sequence 21928, A
Sequence 9, Appli
Sequence 9, Appli
Sequence 117, Ap
Sequence 117, Ap
Sequence 117, Ap
Sequence 117, Ap
Sequence 117, Ap
Sequence 117, Ap
Sequence 117, Ap
Sequence 117, Ap
Sequence 117, Ap
Sequence 1185, Ap
Sequence 2181, Ap
Sequence 2551, Ap
Sequence 2551, Ap
Sequence 2551, Ap
Sequence 8, Appli
Sequence 9524, Ap
Sequence 9524, Ap
Sequence 9524, Ap
Sequence 9524, Ap
Sequence 9525, Ap
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Result

Score

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702.4 461.4 406.4 402.4 402.4 337 241.6 225.6

0

Gaps

0

60 60

180

174 172.4 172.4 168.2 150.8 138.4 138.4

	1260	1201 TGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTGCTG
	1200	
	1200	1 CCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGT
	1140 1140	1081 TGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGCTGCCGAGAAT
	1080	1021 TGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGGAAGCTCTGTGTTCCGGCCA
	1020 1020	961 GGGTTTATAAGAAGTATCCAAACGTGTTTAAGAAGATCCGAGGCATTGTGGAAGAGAGCG
	960 _.	901 TGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATGATGGGGGAGACTTAACCCACT
	900	841 CAGTGTTCGCTTGGAAGGGCGAGTCAGAAGATGACTTCTGGTGGTGTATTGACCGCTGTG
	840	781 CTTGTAACATCTACTCAACTCAGAATGAAGTAGCTGCAGCACTGGCTGAGGCTGGAGTTG
	780 780	721 CCCAGACAGCGGTGTTGATTGAGACACTCTGTGCCCTGGGGGCTCAGTGCCGCTGGTCTG
	720	661 GTGCTCAGGGGGAGAAGCCCTTGGCTGGTGCTAAAATAGTGGGCTGTACACACATCACAG
·	660	601 GACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAAC
	600	541 AAACCAACTCCAAGGGCAGCAGCAGTTTCTGTGTGAAGAACATCAAGCAGGCAG
	540 540	481 GTTCAGCTGCATCCTACACAGATAGCTCTGATGATGAGGTTTCTCCCCGAGAGAAGCAGC
	480	421 CCAAAACTGGCCGAAGATCTTTGTCTCGCTCGATCTCACAGTCCTCCACTGACAGCTACA
	420 420	361 AGGCGCCCAAGAAGCAAATCCAGTTTGCTGATGACATGCAGGAGTTCACCAAATTCCCCA
	360 360	301 TGAAGCAGGCCAAGGAGATCGAGGACGCCGAGAAGTACTCCTTCATGGCCACCGTCACCA
-	300	241 GGGCCGGCGGGGAATGTCGATGCCTGACGCGATGCCCGCTGCCCGGGGTCGGGGAGGAGGAGC
	240 240	181 GGGCAGGCGGGCGGGCGCCAGAGGGGGAAAGAGGCGGGGGG
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US-09-925-300-439
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                                                                                                                 US-09-925-300-439
                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 439
LENGTH: 721
TYPE: DNA
Query Match
Best Local Similarity
Matches 703; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/925,300 CURRENT FILING DATE: 2001-08-10 PRIOR APPLICATION NUMBER: PCT/US00/05988 PRIOR FILING DATE: 2000-03-08 PRIOR APPLICATION NUMBER: 60/124,270 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIOR FILING DATE: 1999-03-12 PRIO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Craig Rosen,
APPLICANT: Steve Ruben
TITLE OF INVENTION: Nucleic
FILE REFERENCE: PA101
                                                                                                                                                                   NAME/KEY: misc feature LOCATION: (688)
                                                                                                                                                                                                                            ORGANISM: Homo sapiens FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1801
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6; Mismatches
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DB 10;
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FILE REFERENCE: 210121.497
CURRENT APPLICATION NUMBER: US/09/867,701
CURRENT FILING DATE: 2001-05-29
NUMBER OF SEQ ID NOS: 10912
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2023
LENGTH: 553
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                            RESULT 3
US-09-867-701-2023
                                                                                                                                                                                                                                                                                                                      Sequence 2023, Application Patent No. US20020132237A1 GENERAL INFORMATION:
FEATURE:

NAME/KEY: misc_feature
LOCATION: (1)...(553)
OTHER INFORMATION: n = I
                                                                                                                                                                                                                             APPLICANT: Aglate, Paul A.
APPLICANT: Jones, Robert
APPLICANT: Harlocker, Susan L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF OVARIAN CANCER
                                                                        ORGANISM: Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                               GACGCCGGGAGATTGAGATTGCAGAGCAAGACATGTCTGCTCTGATTTCACTCAGGAAAC 660
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NUMBER OF SEQ ID NOS: 850

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 850

LENGTH: 636

TYPE: DNA

ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 850, Application US/09879536 Patent No. US20020144298A1
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                                                                                                       TITLE OF INVENTION: PRODUCTS
FILE REFERENCE: CCD-257 (US)
CURRENT APPLICATION NUMBER: US/09/879,536
CURRENT FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/088,801
PRIOR FILING DATE: 1998-06-10
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                                                                                                                                                                                              TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE TITLE OF INVENTION: PRODUCTS
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                                                                                                                                                                                                                                    PPLICANT:
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                                                                                                                                                                                                                                Ford, Donna M.
Lewis, Marcia E.
Monahan, John E.
Schlegel, Robert
                                                                                                                                                                                                                                                                                                              carroll III, Eddie Catino, Theodore J.
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Pred. No. 6.2e-134;
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; OTHER INFORMATION: n =
US-09-879-536-850
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US-09-925-301-217
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                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 217
LENGTH: 2200
                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 217, Application US/09925301 Patent No. US20020052308A1
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Best Local Similarity
Matches 418; Conserv
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CURRENT FILLING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
                                                                                                             NAME/KEY: misc_feature
LOCATION: {{2188}}
OTHER INFORMATION: n equals a,t,9, or
09-925-301-217
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TITLE OF INVENTION: Nucleic Acids, Proteins
FILE REFERENCE: PA106
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Pred. No. 1.1e-116;
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US-10-044-090-344
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CURRENT FILING DATE: 2002-01-09
NUMBER OF SEQ ID NOS: 850
SOFTWARE: PERL Program
SEQ ID NO 344
LENGTH: 2429
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Best Local Similarity 58.4%;
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TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
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ORGANISM: Homo sapiens
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                                                                                                                                                                                    TGTGGTGCATTGAGCAGACCCTGTACTTCAAGGACGGGCCCCTCAACATGATTCTGGACG
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                                                                                                                                                                                                           GGTGGTGTATTGACCGCTGTGTGAACATGGATGGGTGGCAGGCCAACATGATCCTGGATG
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                                                                                                                                                                                                                                                                                CACTGGCTGAGGCTGGAGTTGCAGTGTTCGCTTGGAAGGCCGAGTCAGAAGATGACTTCT
                                                                                                                                                                                                                                                                                                                 GTGCTGAGGTGCAGTCCAGCTGCAACATCTTCTCCACCCAGGACCATGCGGCGGCTG
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GGATCCTCAAGGTGCCTGCCATCAATGTCAATGACTCCGTCACCAAGAGCAAGTTTGACA
                             GGAAGCTCTGTGTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATA 1119
                                                            GAGGCATCTCTGAGGAGACCACGACTGGGGTCCACAACCTCTACAAGATGATGGCCAATG
                                                                                       GAGGCATTGTGGAAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTG 1059
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Pred. No. 4e-115;
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CURRENT APPLICATION NUMBER: US/09/880,107
CURRENT FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR FILING DATE: 2000-06-14
PRIOR APPLICATION NUMBER: US 60/237,054
PRIOR FILING DATE: 2000-10-02
NUMBER OF SEQ ID NOS: 3950
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 346

TITLE OF INVENTION: Gene Expression Profiles FILE REFERENCE: 44921-5028-WO

'n

Liver Cancer

Gene Logic, Inc. Vockley, Jos Scherf, Uwe

Joseph

US-09-880-107-346

Sequence 346, Application US/09880107 Patent No. US20020142981A1

GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Josep

APPLICANT: APPLICANT:

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                                                                                                                                                                                      TGGATGAATACGTTGCCAGCTTGCATCTGCCATCATTTGATGCCCACCTTACAGAGCTGA 1776
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                                  ACAGATAC 1844
                                                                                                                CAGATGACCAAGCAAAATATCTGGGACTCAACAAAAATGGGCCATTCAAACCTAATTATT 1836
                                                                                                                                                                                                                                                                    AACTCTATAATGCACCCGAGGGGGGATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAA 1716
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ACCECTAC 1372
                                                                          CTGAGAAGCCAAGCCCAGTACCTGGGCATGTCCTGTGATGGCCCCCTTCAAGCCGGATCACT 1364
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; OTHER INFORMATION: Genbank Accession No. US20020142981A1 AA157401
US-09-880-107-346
                                                                                                                                                                          PRIOR APPLICATION NUMBER: US 60/176,444
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1461
                                                                  Query Match
Best Local Similarity
                                                        Matches 490;
                                                                                                          TYPE: DNA
ORGANISM: "Unknown
FEATURE: 67
OTHER INFORMATION: Nucleotide sequence encoding
-09-759-990-1
                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: AntiCancer, Inc.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/09759990 Patent No. US20020119491A1
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Best Local Similarity
Matches 381; Conserv
                                                                                                                                                                                                                                                TITLE OF INVENTION: HIGH EXPRESSION AND PRODUCTION OF HIGH TITLE OF INVENTION: SPECIFIC ACTIVITY RECOMBINANT S-ADENOSYLHOMOCYSTAINASE TITLE OF INVENTION: (SAHH) AND IMPROVED ASSAYS FOR S-ADENOSYLMETHIONINE (SFELLE REFERENCE: 31276-20026.00 CURRENT APPLICATION NUMBER: US/09/759,990 CURRENT FILLING DATE: 2001-01-12
                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                1002 GGCATTGTGGAAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCAAAGCTGGG 1061
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ORGANISM: Homo sapiens
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GGTGTTTCCGAAGAGACAACAACAGGTGTCCACCGCCTCTACCAGCTCGAGAAGGAGGGC 672
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Han, Oinghong
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                                                   Score 241.6; DB 10;
Pred. No. 6.2e-65;
0; Mismatches 349;
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                                                                               Length 1461;
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OZAKI,
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Sequence 836, Application US/09738626
Publication No. US20020197605A1
GENERAL INFORMATION:
APPLICANT: NAKAGAWA, SATOSHI
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                                                       YOKOI, HARUHIKO
TATEISHI, NAOKO
SENOH, AKIHIRO
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OCHIAI, KEIKO
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PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
PRIOR FILING DATE: 2000-04-07
PRIOR APPLICATION NUMBER: JP 00/280988
PRIOR FILING DATE: 2000-08-03
NUMBER OF SEQ ID NOS: 7059
SOFTWARE: Patentin ver. 3.0
SEQ ID NO 836
LENGTH: 1422
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US-09-738-626-836
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Matches 477; Conserv
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CURRENT FILING DATE: 2000-12-18
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                                           TACGTTGCCAGCTTGCATCTGCCATCATTGATGCCCACCTTACAGAGCTGACAGATGAC 1784
                                                                                                                                                                                                              CCCACCTTTGTTCTGTCCATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTAT 1664
                                                                                                                                                                                                                                                                                  CGCTCCATCATCGTCCTGTCCGAAGGTCGCCTGTTGAACCTTGGCAACGCCACCGGACAC 1185
                                                                                                                                                                                                                                                                                                                                                                       GACGACGTCACCCGCACCACGATCAAGCCACAGGTCGACGAGTTCACCTTCTCCACCGGT 1125
                                                                                                                                                                                                                                                                                                                                                                                                                     CCGGAGCTGACGTGGGAGCGAGTACGTTCTCAGGTGGACCATGTCATCTGGCCAGATGGC 1547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGCTGGGCAACATCGGTCACTTTGATAATGAGATCGATATGCATTCCCTGTTGCACCGC 1065
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                                                                                            CA----AAACGAAGGACAGTACGAGAACGAGGTCTACCGTCTGCCTAAGGTTCTCGACGAA
                                                                                                                                        AATGCACCCGAGGGGCGATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAA 1724
                                                                                                                                                                                      CCATCATTTGTCATGTCCAACTCTTTCGCCGATCAGACCATTGCGCAGATCGAACTGTTC
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; OTHER INFORMATION: RXN00132
US-09-746-660A-97
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SOFTWARE: Paten
SEQ ID NO 97
SEQTH: 1557
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Publication No.
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Matches 47
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Best Local Si
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TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS.
FILE REFERENCE: BGI-121CP2
CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT FILING DATE: 2000-12-22
CURRENT FILING DATE: 2000-12-22
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/141031 PRIOR FILING DATE: 1999-06-25
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/148613
PRIOR FILING DATE: 1999-08-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILING DATE: 2000-06-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/603124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Corynebacterium glutamicum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1785 CAAGCAAAATATCTGGGACTCAACAAAAATGGGCCATTCAAACCTAATTATTACAGATAC 1844
                                                                                                                                                                                                                                           1071
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                                                                                 1191
                                                                                                                                                              1131
                                                                                                                                                                                                                                                                                                       1011 GAAGAGAGCGTGACTGGTGTTCACAGGCTGTATCAGCTCTCCCAAAGCTGGGAAGCTCTGT 1070
  1251 CTTGGAGCAATTGTCTACATTACCGAAATCGACCCCATCTGTGCTCTGCAGGCCTGCATG 1310
                                                                                                                        818
                                                                                                                                                                                                   758 TTCCCAGCGATGAACGTCAACGACGCTGTCACCAAGTCCAAGTTTGATAACAAGTACGGC
                                                                                                                                                                                                                                                                                  698 GAGGAAACCACCACCGGTGTGCACCGCCTGTACCACTTCGCTGAAGAAGGCGTGCTGCCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 1999-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: DE 19931420.9
FILING DATE: 1999-07-08
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/187970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 60/142101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 2000-03-09
                                                                               CAAGTGGTGGTGTGTGGCTATGGTGAGGTAGGCAAGGGCTGCTGTGCTGCTCTCAAAGCT 1250
                                                                                                                                                            TGCCGAGAATCCATTTTGGATGGCCTGAAGAGGACCACAGATGTGATGTTTGGTGGGAAA 1190
                                                                                                                                                                                                                                           GTTCCGGCCATGAACGTCAATGATTCTGTTACCAAACAGAAGTTTGATAACTTGTACTGC 1130
                                       ACCCGCCACTCCCTGATCGACGGCATCAACCGCGCCACTGACATGCTCATGGGCGGCAAG 877
                                                                                                                                                                                                                                                                                                                                                                  477;
                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim, Jun-Won
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zelder, Oskar
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                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                Score 225.6; DB 9;
Pred. No. 6.5e-60;
0; M1smatches 354;
                                                                                                                                                                                                                                                                                                                                                                                                     Length 1557;
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0S-10-021-121-1/c
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Patent No. US20020142444A1
GENERAL INFORMATION:
     INFORMATION FOR
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                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/635,130

APPLICATION NUMBER: US/08/635,130

APPLICATION NUMBER: US/08/635,130

APPLICATION INDEE: 1966

ATTORNEY/AGENT INFORMATION:

NAME: TOICHIA, PhD. Timothy E.

REGISTRATION NUMBER: 36,700

REFERENCE/DOCKET NUMBER: P1001

TELEPHONE: 650/252-8674

TELEPHONE: 650/252-8674

TELEPHONE: 650/252-9881
                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb i
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
                                                                                                                                                                                                                                                                                                                                                         CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: A2-1 Neurotrophic Factor NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGCTGAGTACATCGGCGTTGACGTTGCAGGCCCATTCAAGCCGGAGCACTACCGCTAC
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                                                                                                                                                                                                                                                                        NT APPLICATION DATA:
APPLICATION NUMBER: US/10/021,121
FILING DATE: 06-Dec-2001
GLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Genentech, Inc
STREET: 1 DNA Way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94080
                                                                                                                                                                                                                                                                                                                                                                                                                                                        inch, 1.44 Mb floppy disk
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US-09-746-660A-101
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Best Local Similarity
Matches 190; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 101,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Publication No.
                                                                                                                                                                                                                                                              APPLICANT: Hwang, Byung-Joon
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
TITLE OF INVENTION: METABOLIC PATHWAY PROTEINS
FILE REFERENCE: BGI-1210P2
CURRENT APPLICATION NUMBER: US/09/746,660A
CURRENT FILING DATE: 2000-12-22
                                                                                                                                                                                          PRIOR APPLICATION NUMBER: 09/606740
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 09/603124
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                                                                                                                   FILING DATE: 2000-06-23
APPLICATION NUMBER: 60/141031
FILING DATE: 1999-06-25
                                       APPLICATION NUMBER: 60/142101
FILING DATE: 1999-07-02
APPLICATION NUMBER: 60/148613
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
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STRANDEDNESS: Double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Extra Cellular LOCATION: 244-899 IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: Linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IDENTIFICATION METHOD:
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244-321
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60/187970
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Pred. No.
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. 9.8e-49;
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US-09-738-626-838/c
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; LOCATION: (101)..(1396)
; OTHER INFORMATION: FRXA
US-09-746-660A-101
                                                                             Sequence 838, Application US/09738626 Publication No. US20020197605A1 GENERAL INFORMATION:
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Best Local Similarity
Matches 377; Conserv
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SEQ ID NO 101
LENGTH: 1396
                                     APPLICANT: NAKAGAWA, SATOSHI APPLICANT: MIZOGUCHI, HIROSI
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PRIOR APPLICATION NUMBER: DE
PRIOR FILING DATE: 1999-07-08
NUMBER OF SEQ ID NOS: 125
  APPLICANT:
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                                                                                                                                                                                                                                                         1608 ACC---TTTGTTCTGTCCATCACAGCCACAACACAGGCTTTTGGCACTGATAGAACTCT 1662
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                                                                                                                                                                                                                                                                                                                       CGCTCCATCATCGTCCTGTCCGAAGGTCGCCTGTTGAACCTTGGCAACGCCACCGGACAC
MIZOGUCHI, HIROSHI
ANDO, SEIKO
HAYASHI, MIKIRO
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Pred. No. 1.5e-47;
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Patent No. USANCION:
GENERAL INFORMATION:
APPLICANT: Monsanto Co
APPLICANT: Concibido, Vergel
APPLICANT: Concibido, Vergel
APPLICANT: Delanney, Xavier
INTILE OF INVENTION: Socreening of Soybean Plants with Enhanced Yields
INTILE OF INVENTION: Socreening of Soybean Plants with Enhanced Yields
INTILE OF INVENTION: Socreening of Soybean Plants with Enhanced Yields
INTILE OF INVENTION: Socreening of Soybean Plants with Enhanced Yields
INTILE OF INVENTION: US/10/037,598
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US-10-037-598-26
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                                                                                                                                                                                                                         Sequence 26, Application US/10037598 Patent No. US20020157143A1
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Best Local Similarity
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LENGTH: 720
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CURRENT APPLICATION NUMBER: US/09/738,626
CURRENT FILING DATE: 2000-12-18
PRIOR APPLICATION NUMBER: JP 99/377484
PRIOR FILING DATE: 1999-12-16
PRIOR APPLICATION NUMBER: JP 00/159162
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SOFTWARE: Patentin
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PRIOR APPLICATION NUMBER: JP 00/280988
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APPLICANT: OZAKI, AKIO
TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
FILE REFERENCE: 249-125
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Pred. No. 5.9e-44;
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PRIOR APPLICATION NUMBER: 06/260,040
PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin version 3.0
SEQ ID NO 26
LENGTH: 3830
TYPE: No. 2
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RESULT 15
US-09-754-853A-4/c
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; ORGANISM: Glycine
US-10-037-598-26
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                                                                       CAGTGTGCCTGTTGAGGGTCCATACAAGCCTGCTCACTACAGGTAC
                                                                                                                                   TCACETGGGCAAACTTGGAGCTAAGCTGACCCAGCTTAGCAAGTCCCAGGCTGATTACAT
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                                                                                                       GGGACTCAACAAAATGGGCCATTCAAACCTAATTATTACAGATAC 1844
                                                                                                                                                                                                                  CAAGTACGAGAAGAAGGTTTACGTTTTGCCCCAAGCACCTTGATGAGAAGGTGGCTGCACT
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Sequence 4, Application US/09754853A Publication No. US20030005491A1 GENERAL INFORMATION:

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; OTHER INFORMATION: unsure at
; OTHER INFORMATION: Clone ID:
US-09-754-853A-4
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LENGTH: 513509
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: Nucleic Acid Molecules
TITLE OF INVENTION: Soybean Cyst Nematode
FILE REFERENCE: 38-10(15810)B
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LOCATION: (111805)..(113968),(114684)..(115204)
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  CAAGTACGAGAAGAAGGTTTACGTTTTGCCCAAGCACCTTGATGAGAAGGTGGCTGCACT
                        GCGATACAAGCAGGATGTGTACTTGCTTCCTAAGAAAATGGATGAATACGTTGCCAGCTT
                                                                                                               CATCACAGCCACAACACAGGCTTTGGCACTGATAGAACTCTATAATGCACCCG---AGGG
                                                                                                                                                                                                            GGCAGAGGGTCGTCTACTCAATTTGAGCTGCTCCACAGTTCCCCACC---TTTGTTCTGTC
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                                                                                CTGCTCCTTCACCAACCAGGTCATTGCTCAGCTTGAGTTGTGGAAGGAGAAGAGTACCGG
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Parnell, Laurence D.
Parsons, Jeremy D.
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Pred. No. 6.6e-42;
0; Mismatches 331;
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Search completed: April 21, 2003, 07:45:05 Job time: 1204.11 secs

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